MycoKeys 114: 177–212 (2025)
DOI: 10.3897/mycokeys.114.145368

Research Article

Morphological characteristics and phylogenetic analyses revealed five new species (Basidiomycota) from Southwestern China

Ali Yang[1,2*], Lu Wang[3*], Yongjun Hu[2], Yingtao Jiang[1,2], Guiying Shi[1], Changlin Zhao[3]

1 *College of Horticulture, Gansu Agricultural University, Lanzhou 730000, China*
2 *Department of Edible Fungi, Institute of Biology, Gansu Academy of Sciences, Lanzhou 730000, China*
3 *College of Forestry, Southwest Forestry University, Kunming 650224, China*

Corresponding author: Guiying Shi (shigy@gsau.edu.cn); Changlin Zhao (fungi@swfu.edu.cn)

Abstract

In the present study, five new wood-inhabiting fungal species, *Conferticium albocremeum* (Stereaceae, Russulales), *Dendrocorticiopsis luteoalba* (Punctulariaceae, Corticiales), *Eichleriella biluoxueshanensis* (Auriculariaceae, Auriculariales), *Gloeohypochnicium yunnanense* (Incertae sedis, Russulales), and *Punctularia nigrodontea* (Punctulariaceae, Corticiales), collected from southern China, are proposed based on a combination of morphological features and phylogenetic evidence. *Conferticium albocremeum* is characterized by membranaceous and smooth basidiomata with white to cream surface and ellipsoid and verrucose basidiospores (9–11 × 5–7 µm); *Dendrocorticiopsis luteoalba* is characterized white to buff, membranaceous basidiomata and ellipsoid, thin-walled and smooth basidiospores (7–8 × 4.5–5.5 µm); *Eichleriella biluoxueshanensis* is characterized by coriaceous and grandinioid basidiomata with buff to cinnamon-buff hymenophore and allantoid, thin-walled basidiospores (13.5–17.5 × 7–9 µm); *Gloeohypochnicium yunnanense* is characterized by buff to cream, coriaceous and smooth basidiomata and globose, thick-walled and warted basidiospores (10–12 × 10–11.5 µm), and *Punctularia nigrodontea* is characterized by resupinate to effused-reflexed basidiomata and ellipsoid, thin-walled and smooth basidiospores (8.5–10 × 5–6 µm). Sequences of the internal transcribed spacers (ITS) and the large subunit (nLSU) of the nuclear ribosomal DNA (rDNA) markers of the studied samples were generated. Phylogenetic analyses performed based on the ITS+nLSU rDNA gene regions with the maximum likelihood, maximum parsimony, and Bayesian inference methods revealed that five new species belong to the genera *Conferticium*, *Dendrocorticiopsis*, *Eichleriella*, *Gloeohypochnicium*, and *Punctularia*. Descriptions, illustrations, phylogenetic analysis results, and a comparison with closely related taxa of the five new species are provided.

Key words: Biodiversity, molecular systematics, new taxa, taxonomy, wood-inhabiting fungi, Yunnan Province

OPEN ACCESS

This article is part of:
Exploring the Hidden Fungal Diversity: Biodiversity, Taxonomy, and Phylogeny of Saprobic Fungi
Edited by Samantha C. Karunarathna, Danushka Sandaruwan Tennakoon, Ajay Kumar Gautam

Academic editor:
Samantha C. Karunarathna
Received: 26 December 2024
Accepted: 28 January 2025
Published: 28 February 2025

Citation: Yang A, Wang L, Hu Y, Jiang Y, Shi G, Zhao C (2025) Morphological characteristics and phylogenetic analyses revealed five new species (Basidiomycota) from Southwestern China. MycoKeys 114: 177–212. https://doi.org/10.3897/mycokeys.114.145368

Copyright: © Ali Yang et al.
This is an open access article distributed under terms of the Creative Commons Attribution License (Attribution 4.0 International – CC BY 4.0).

* These authors have contributed equally to this work and share the first authorship.

Introduction

The kingdom of fungi is one of the most diverse groups of living organisms on earth; its members occur across a broad range of ecosystems, including extreme environments, with an estimated number of species in the range of 2–3 million (Bhunjun et al. 2022, 2024; Wijayawardene et al. 2022, 2024; Dong et al. 2024a; Hyde et al. 2024a, b). Based on molecular phylogenetic evidence, numerous new taxa have been discovered in the past ten years (Wang and Cai 2023; Yuan et al. 2023; Zhao et al. 2023; Deng et al. 2024b; Dong et al. 2024b; He et al. 2024; Qin et al. 2024).

The genus *Conferticium* Hallenb. (Stereaceae, Russulales) was erected in 1980 and typified by *C. insidiosum* (Bourdot & Galzin) Hallenb., which is characterized by the resupinate basidiomes with membranaceous to ceraceous, smooth to tuberculate hymenophore, a monomitic simple-septate hyphae, and the numerous cylindrical, sinuous gloeocystidia (Bernicchia and Gorjón 2010). Based on the MycoBank database (http://www.mycobank.org, accessed on 27 January 2025) and the Index Fungorum (http://www.indexfungorum.org, accessed on 27 January 2025), six specific and infraspecific names were registered in *Conferticium*, and it is a small genus only including five widely recognized species up to now.

The genus *Dendrocorticiopsis* Sheng H. Wu et al. (Punctulariaceae, Corticiales) was introduced by Sheng H. Wu, with the description of one species, *D. orientalis* Sheng H. Wu et al. (Wei et al. 2022). It is conventionally defined by having strictly resupinate basidiomata, an ivory hymenophore, a monomitic hyphal system with clamped hyphae, encrusted cystidia, dendrohyphidia, and ellipsoid to ovoid basidiospores (Wei et al. 2022). Based on the MycoBank database (http://www.mycobank.org, accessed on 27 January 2025) and the Index Fungorum (http://www.indexfungorum.org, accessed on 27 January 2025), *Dendrocorticiopsis* is a monotypic genus.

The genus *Eichleriella* Bres. was introduced in 1903, typified by *E. incarnata* Bres., and it is a species-rich genus that belongs to Auriculariaceae (Auriculariales). The genus is characterized by annual or short-living perennial, leathery to ceraceous basidiomata with smooth, pale-colored hymenophore (in some species covered by spines), a monomitic to dimitic hyphal system with clamped genitive hyphae, cystidia often present, longitudinally septate basidia with 2- or 4-celled, and colorless, cylindrical to narrowly cylindrical basidiospores (Malysheva and Spirin 2017; Li et al. 2023; Deng et al. 2024a). Based on the MycoBank database (http://www.mycobank.org, accessed on 27 January 2025) and the Index Fungorum (http://www.indexfungorum.org, accessed on 27 January 2025), the genus *Eichleriella* has 32 specific and registered names, with 22 species accepted worldwide (Malysheva and Spirin 2017, Liu et al. 2019, Li et al. 2023; Deng et al. 2024a).

The genus *Gloeohypochnicium* (Parmasto) Hjortstam (Russulales), typified by *G. analogum* (Bourdot & Galzin) Hjortstam (Bernicchia and Gorjón 2010), is characterized by the resupinate basidiomes with smooth to tuberculate hymenophore, a monomitic hyphal system with clamps on generative hyphae, the numerous cylindrical, sinuous gloeocystidia, and globose to ellipsoid, thick-walled, warted basidiospores (Bernicchia and Gorjón 2010). Based on the MycoBank database (http://www.mycobank.org, accessed on 27 January 2025) and the Index Fungorum (http://www.indexfungorum.org, accessed on 27 January 2025), *Gloeohypochnicium* has registered two specific and infraspecific

names, and it is a small genus only including two widely recognized species so far (Bernicchia and Gorjón 2010; He et al. 2024).

Punctularia Patouillard (Punctulariaceae, Corticiales) was typified with *P. tuberculosa* (Pat.) Pat. & Lagerh. (current name *P. atropurpurascens* (Berk. & Broome) Petch, which is characterized by resupinate to effused-reflexed basidiomata, gelatinous when fresh, rigid upon drying, tuberculate or radial ridges hymenophore, a monomitic hyphal system with clamped generative hyphae, yellowish to brown dendrohyphidia, and thin-walled, smooth, ellipsoid, acyanophilous basidiospores (Bernicchia and Gorjón 2010). Based on the MycoBank database (http://www.mycobank.org, accessed on 27 January 2025) and the Index Fungorum (http://www.indexfungorum.org, accessed on 27 January 2025), *Punctularia* has registered six specific and infraspecific names, and three species have been recognized worldwide up to now (Bernicchia and Gorjón 2010; Guan et al. 2021; He et al. 2024).

Molecular phylogenetic approaches have revolutionized the fungal taxonomy of Basidiomycota in the last decades, and these advances have greatly enhanced our knowledge of species diversity in Basidiomycota (Lücking et al. 2021; He et al. 2022; Wang et al. 2023; Dong et al. 2024a). The family Auriculariaceae is the largest and best-supported clade in the order Auriculariales and consists of a large group of wood-decaying fungi with varied basidiomes (Dong et al. 2024b; He et al. 2024). Corticioid and stereoid taxa are numerous in Auriculariaceae and are typically classified into three main genera: *Eichleriella* Bres., *Exidiopsis* (Bref.) A. Møller, and *Heterochaete* Pat. (Malysheva and Spirin 2017; Li et al. 2023; Deng et al. 2024a). DNA sequence-based classification and identification of the genus *Eichleriella* (Auriculariaceae) have reported that six species have been described from China recently (Li et al. 2023; Deng et al. 2024a). Corticiales K.H. Larss. is a small order of corticioid fungi with four families *viz*. Corticiaceae Herter, Dendrominiaceae Ghobad-Nejhad, Punctulariaceae Donk, and Vuilleminiaceae Maire ex Lotsy (Wei et al. 2022; He et al. 2024). Most of the previous studies of Punctulariaceae focused on European species (Bernicchia and Gorjón 2010; Gorjón and Bernicchia 2017). In China, the research on this family mainly focuses on the genera *Dendrocorticiopsis* and *Punctularia*; some new taxa have been proposed based on a combination of morphological features and molecular data (Guan et al. 2021; Wei et al. 2022; He et al. 2024). Members of the Russulales Kreisel ex P.M. Kirk, P.F. Cannon & J.C. David exhibit diverse basidiome structures, which can range from agaricoid to discoid, clavarioid, polyporoid, corticoid, and even gasteroid, and the multigene phylogenetic analyses clarify the evolutionary relationships of some small genera in the latest study (Yuan et al. 2021; He et al. 2024). According to recent research in molecular systematics, the genus *Conferticium* (Stereaceae, Russulales) has reported one new species, *C. fissuratum* Xin Yang & C.L. Zhao from Yunnan Province (Bernicchia and Gorjón 2010; Shen et al. 2024). The taxonomic status of the genus *Gloeohypochnicium* is unclear, and it was only placed in the order Russulales, and it is a mystery genus; no new taxa in the genus have been described for nearly a decade (He et al. 2022, 2024). However, the phylogeny of the genus *Gloeohypochnicium* is ambiguous due to a lack of molecular evidence and morphological data.

In this paper, we presented the morphological characteristics and multigene molecular analyses with ITS and nLSU DNA markers to support the taxonomy and phylogenetic position of five new species.

Materials and methods

Sample collection and herbarium specimen preparation

Fresh basidiomata growing on angiosperm branches were collected from Dehong, Diqing, Tengchong, and Xishuangbanna of Yunnan Province, P.R. China. The samples were photographed *in situ*, and fresh macroscopic details were recorded. Photographs were recorded using a Jianeng 80D camera (Tokyo, Japan). Specimens were dried in an electric food dehydrator at 45 °C (Hu et al. 2022), then the specimens were sealed in an envelope and zip-lock plastic bags and labeled (Zhao et al. 2023). The dried specimens were deposited in the herbarium of the Southwest Forestry University (SWFC), Kunming, Yunnan Province, China.

Morphology

The macromorphological descriptions were based on field notes and photos captured in the field and lab. The color terminology follows Petersen (1996). The micromorphological data were obtained from the dried specimens observed under a Nikon Eclipse E100 light microscope following Zhao and Wu (2017). The following abbreviations are used: KOH = 5% potassium hydroxide water solution, CB– = acyanophilous, IKI+ = amyloid, IKI– = both inamyloid and indextrinoid, L = mean spore length (arithmetic average for all spores), W = mean spore width (arithmetic average for all spores), Q = variation in the L/W ratios between the specimens studied, and n = a/b (number of spores (a) measured from given number (b) of specimens).

DNA extraction, PCR, and sequencing

The CTAB rapid plant genome extraction kit-DN14 (Aidlab Biotechnologies Co., Ltd., Beijing, China) was used to obtain genomic DNA from the dried specimens according to the manufacturer's instructions. The nuclear ribosomal internal transcribed spacer (ITS) region was amplified with the primer pair ITS5/ITS4 (White et al. 1990). The nuclear large subunit (nLSU) region with the primer pair LR0R/LR7 (Vilgalys and Hester 1990). The PCR procedure for ITS was as follows: initial denaturation at 95 °C for 3 min, followed by 35 cycles at 94 °C for 40 s, 58 °C for 45 s, and 72 °C for 1 min, and a final extension of 72 °C for 10 min. The PCR procedure for nLSU was as follows: initial denaturation at 94 °C for 1 min, followed by 35 cycles at 94 °C for 30 s, 48 °C for 1 min, and 72 °C for 1.5 min, and a final extension of 72 °C for 10 min. The PCR products were purified and sequenced at Kunming Tsingke Biological Technology Limited Company (Yunnan Province, P.R. China). All newly generated sequences were deposited in GenBank (Table 1).

Molecular phylogeny

The sequences were aligned in MAFFT version 7 using the G-INS-i strategy (Katoh et al. 2019). The alignment was adjusted manually using AliView version 1.27 (Larsson 2014). (1) *Hyphoderma cremeoalbum* (Höhn. & Litsch.) Jülich was assigned as an outgroup to root trees in the ITS+nLSU analysis (Fig. 1) (Dong et al. 2024a); (2) *Vararia fissurata* Y.L. Deng & C.L. Zhao were

Table 1. Names, voucher numbers, references, and corresponding GenBank accession numbers of the taxa used in the phylogenetic analyses. [* indicates type materials; – indicates sequence unavailability].

Taxa	Voucher no.	Locality	GenBank accession no.		References
			ITS	nLSU	
Acanthobasidium bambusicola	He2357	China	KU559343	KU574833	Tian et al. 2018
Acanthobasidium phragmitis	CBS 233.86	France	–	AY039305	Wu et al. 2001
Acanthophysium bisporum	T614	USA	–	AY039327	Maekawa et al. 2023
Acanthophysium lividocaeruleum	FP-100292	USA	–	AY039319	Maekawa et al. 2023
Adustochaete punctata	CLZhao 29675	China	PP852052	PP849035	Dong et al. 2024b
Aleurobotrys botryosus	He2712	China	KX306877	KY450788	Tian et al. 2018
Aleurodiscus bambusinus	He4261	China	KY706207	KY706219	Tian et al. 2018
Alloexidiopsis australiensis	LWZ 20180514-18	China	OM801934	OM801919	Liu et al. 2022
Alloexidiopsis calcea	LWZ 20180904-14	China	OM801935	OM801920	Liu et al. 2022
Alloexidiopsis grandinea	CLZhao 33798	China	PP852058	–	Dong et al. 2024b
Alloexidiopsis xantha	CLZhao 25093	China	PP852060	PP849040	Dong et al. 2024b
Alloexidiopsis yunnanensis	CLZhao 8106	China	MT215569	MT215565	Guan et al. 2020
Amphistereum leveilleanum	FP-106715	USA	KX262119	KX262168	Malysheva and Spirin 2017
Amphistereum schrenkii	HHB 8476	USA	KX262130	KX262178	Malysheva and Spirin 2017
Amylostereum chailletii	NH 8031	–	AF506406	AF506406	Larsson and Larsson 2003
Amylostereum laevigatum	NH 12863	–	AF506407	AF506407	Larsson and Larsson 2003
Aporpium caryae	Miettinen 14774	Finland	JX044145	–	Miettinen et al. 2012
Aporpium caryae	WD 2207	Japan	AB871751	AB871730	Sotome et al. 2014
Artomyces niveus	CLZhao 19094	China	OR094479	OR461459	Dong et al. 2024a
Artomyces yunnanensis	CLZhao 7118	China	OR094476	OR461461	Dong et al. 2024a
Auricularia auricula-judae	JT 04	UK	KT152099	KT152115	Tohtirjap et al. 2023
Auricularia cornea	Dai 13621	China	MZ618936	MZ669905	Tohtirjap et al. 2023
Auricularia mesenterica	FO 25132	Germany	AF291271	AF291292	Weiß and Oberwinkler 2001
Auricularia polytricha	TUFC 12920	Japan	AB871752	AB871733	Sotome et al. 2014
Auricularia tibetica	Dai 13336	China	MZ618943	MZ669915	Tohtirjap et al. 2023
Australovuilleminia coccinea	BCP5551	New Zealand	HM046875	HM046930	Ghobad-Nejhad et al. 2010
Basidiodesertica hydei	SQUCC 15289	Oman	MW077150	MW077159	Wei et al. 2022
Bondarzewia occidentalis	AFTOL-ID 452	Canada	DQ200923	DQ234539	Zhou et al. 2021
Bondarzewia podocarpi	Dai 9261	China	KJ583207	KJ583221	Zhou et al. 2021
Conferticium albocremeum	CLZhao 35693*	China	PQ197729	PQ783842	Present study
Conferticium albocremeum	CLZhao 36343	China	PQ783832	PQ783843	Present study
Conferticium albocremeum	CLZhao 37176	China	PQ783833	PQ783844	Present study
Conferticium albocremeum	CLZhao 39238	China	PQ783834	–	Present study
Conferticium fissuratum	CLZhao 34654	China	PQ201856	–	Shen et al. 2024
Conferticium fissuratum	CLZhao 34662	China	PQ201857	–	Shen et al. 2024
Conferticium heimii	CBS321.66	African	AF506381	AF506381	Tian et al. 2018
Conferticium ochraceum	CLZhao 21515	China	ON211619	–	Present study

Taxa	Voucher no.	Locality	GenBank accession no.		References
			ITS	nLSU	
Conferticium ochraceum	G07_P24A	Switzerland	KT943933	–	Stroheker et al. 2018
Conferticium ravum	CBS:125849	Estonia	MH863805	MH875269	Vu et al. 2019
Conferticium ravum	NH13291	USA	AF506382	AF506382	Larsson and Larsson 2003
Corticium roseum	MG252	China	MW805872	MW805836	Ghobad-Nejhad et al. 2021
Corticium thailandicum	MG242	Tailand	MW805868	MW805831	Ghobad-Nejhad et al. 2021
Cytidia salicina	MG49	Finland	GU590881	HM046921	Wei et al. 2022
Dendrocorticiopsis luteoalba	CLZhao 30380*	China	PQ783828	PQ783838	Present study
Dendrocorticiopsis orientalis	He 4195	China	MW580926	MW580921	Wei et al. 2022
Dendrocorticiopsis orientalis	WEI 20-166	China	MW580922	MW580924	Wei et al. 2022
Dendrocorticium polygonioides	CBS:106.56	France	MH857525	MH869062	Vu et al. 2019
Dendrocorticium roseocarneum	KUC20121109-32	Korea	KJ668559	KJ668413	Ghobad-Nejhad and Duhem 2014
Dendrominia dryina	MG159	France	JX892936	JX892937	Ghobad-Nejhad and Duhem 2014
Dendrominia ericae	MG162	France	JX892938	JX892939	Ghobad-Nejhad and Duhem 2014
Dentipellicula austroafricana	Dai 12580	Africa	KJ855274	KJ855275	Zhou et al. 2021
Dentipellicula taiwaniana	Dai 10867	China	JQ349115	JQ349101	Zhou et al. 2021
Dentipellopsis dacrydicola	Dai 12004	–	JQ349104	JQ349089	Zhou and Dai 2013
Dentipellopsis dacrydicola	Dai 12010	–	–	JQ349090	Zhou and Dai 2013
Disporotrichum dimorphosporum	CBS:419.70	Netherland	MH859776	MH871538	Vu et al. 2019
Disporotrichum dimorphosporum	CBS:433.85	USA	MH861895	MH873584	Vu et al. 2019
Eichleriella alliciens	He4055b	Thailand	MH178244	–	Li et al. 2023
Eichleriella alliciens	HHB 7194	USA	KX262120	KX262169	Malysheva and Spirin 2017
Eichleriella alpina	He 20120916-1	China	MH178245	MH178268	Li et al. 2023
Eichleriella bactriana	TAAM 104431	Uzbekistan	KX262138	KX262186	Malysheva and Spirin 2017
Eichleriella bambusicola	Dai 6391	China	MH178246	–	Li et al. 2023
Eichleriella biluoxueshanensis	CLZhao 34516*	China	PQ783827	PQ783837	Present study
Eichleriella biluoxueshanensis	CLZhao 34793	China	PQ787846	–	Present study
Eichleriella crocata	He2969	China	MH178248	MH178271	Li et al. 2023
Eichleriella crocata	TAAM 101077	Russia	KX262100	KX262147	Malysheva and Spirin 2017
Eichleriella delicata	CLZhao 25143	China	PQ757163	–	Present study
Eichleriella delicata	He3469	China	MH178250	MH178273	Li et al. 2023
Eichleriella desertorum	LR 49350	Namibia	KX262142	KX262190	Malysheva and Spirin 2017
Eichleriella discolor	He4584	China	MH178252	MH178275	Li et al. 2023
Eichleriella discolor	He4763	China	MH178253	MH178276	Li et al. 2023
Eichleriella flavida	LR 49412	UK	KX262137	KX262185	Malysheva and Spirin 2017
Eichleriella leucophaea	LE 303261	Russia	KX262111	KX262161	Malysheva and Spirin 2017

Taxa	Voucher no.	Locality	GenBank accession no.		References
			ITS	nLSU	
Eichleriella macrospora	He2189	USA	MH178251	MH178274	Li et al. 2023
Eichleriella ochracea	SP467242	Brazil	MK391514	–	Alvarenga et al. 2019
Eichleriella shearii	LR 23258	–	KX262139	–	Malysheva and Spirin 2017
Eichleriella shearii	USJ 54609	Costa Rica	AF291284	AF291335	Weiß et al. 2001
Eichleriella sicca	OM 17349	USA	KX262143	KX262191	Malysheva and Spirin 2017
Eichleriella sinensis	CLZhao 29368	China	PQ757164	–	Present study
Eichleriella sinensis	CLZhao 31647	China	PQ757165	PQ757166	Present study
Eichleriella sinensis	He4196	China	MH178254	MH178277	Li et al. 2023
Eichleriella tenuicula	CLZhao 35797	China	PQ197731	–	Present study
Eichleriella tenuicula	He3483	China	MH178256	MH178279	Li et al. 2023
Eichleriella xinpingensis	CLZhao 836	China	MK560879	MK560883	Liu et al. 2019
Eichleriella xinpingensis	CLZhao 842	China	MK560880	MK560884	Liu et al. 2019
Eichleriella yunnanensis	CLZhao 31317	China	PP889850	PP897009	Deng et al. 2024a
Eichleriella yunnanensis	CLZhao 31350	China	PP889852	PP897010	Deng et al. 2024a
Elmerina cladophora	Miettinen 14314	Indonesia	MG757509	MG757509	Malysheva et al. 2018
Elmerina sclerodontia	Miettinen 16431	Malaysia	MG757512	MG757512	Malysheva et al. 2018
Erythricium hypnophilum	MG169	France	MW805858	MW805823	Ghobad-Nejhad et al. 2021
Erythricium laetum	MG72	–	GU590875	GU590878	Ghobad-Nejhad et al. 2021
Exidia candida	VS 3921	Russia	KY801867	KY801892	Spirin et al. 2018
Exidia glandulosa	MW 355	Germany	AF291273	AF291319	Weiß et al. 2001
Exidia pithya	MW 313	Germany	AF291275	AF291321	Weiß et al. 2001
Exidia reflexa	Dai 20833	China	MN850386	MN850362	Ye et al. 2020
Exidia subglandulosa	Wu 270	China	MN850381	MN850357	Ye et al. 2020
Exidiopsis effusa	OM 19136	Finland	KX262145	KX262193	Malysheva and Spirin 2017
Gloeocystidiellum bisporum	KHL11135	Norway	AY048877	AY048877	Larsson and Larsson 2003
Gloeocystidiellum clavuligerum	FCUG2731	Russia	AF310083	AF310083	Larsson and Larsson 2003
Gloeodontia eriobotryae	Dai 12080	–	JQ349116	JQ349103	Zhou and Dai 2013
Gloeodontia pyramidata	LR15502	–	AF506446	AF506446	Larsson and Larsson 2003
Gloeohypochnicium analogum	NZFS:4549	New Zealand	MH409974	–	Hood et al. 2018
Gloeohypochnicium analogum	PDD:91626	New Zealand	GQ411521	–	Fukami et al. 2010
Gloeohypochnicium yunnanense	CLZhao 30018	China	PQ783830	PQ783840	Present study
Gloeohypochnicium yunnanense	CLZhao 30049*	China	PQ783831	PQ783841	Present study
Gloeophyllum abietinum	H 22988	Switzerland	JX524619	KC782733	He et al. 2014
Hericium abietis	NH 6990	Canada	AF506456	AF506456	Zhou et al. 2021
Hericium coralloides	NH 282	Sweden	AF506459	AF506459	Zhou et al. 2021
Heterobasidion annosum	Dai 20962	China	ON417163	ON417213	Liu et al. 2022
Heteroradulum australiense	LWZ 20180512-25	Australia	MZ325255	MZ310425	Li et al. 2022
Heteroradulum degluben	LE 38182	Sweden	KX262112	KX262162	Malysheva and Spirin 2017

Taxa	Voucher no.	Locality	GenBank accession no.		References
			ITS	nLSU	
Heteroradulum kmetii	He 4915	China	MH178262	MH178286	Li et al. 2023
Heteroradulum labyrinthinum	Yuan 1600	China	KM379139	KM379140	Yuan et al. 2018
Heteroradulum mussooriense	Dai 17193	China	MH178265	MH178289	Li et al. 2023
Hyphoderma cremeoalbum	CLZhao 17007	China	OM985716	OM985753	Dong et al. 2024a
Lactarius crocatus	KVP08034	Thailand	HQ318243	HQ318151	Wu et al. 2020
Lactarius deceptivus	AFTOL-ID 682	USA	AY854089	AY631899	Wu et al. 2020
Laetisaria fuciformis	CBS:182.49	Netherlands	MH856485	MH868023	Vu et al. 2019
Laetisaria roseipellis	CBS:299.82	–	EU622846	EU622844	Vu et al. 2019
Lawreymyces palicei	Palice 2509	Ecuador	AY542864	AY542864	Lücking and Moncada 2017
Lawreymyces palicei	Palice 4369	Ecuador	AY542865	AY542865	Lücking and Moncada 2017
Lentinellus sublineolatus	TENN 059307	Austria	NR119505	–	Dong et al. 2024a
Lentinellus vulpinus	7267	Sweden	AY513230	–	Kneal and Smith 2015
Marchandiomyces aurantioroseus	FCUG 1166	Sweden	KP864659	HM046929	Ghobad-Nejhad et al. 2021
Marchandiomyces corallinus	JL128-98	–	AY583327	AY583331	DePriest et al. 2005
Megalocystidium diffissum	V.Spirin4244	Sweden	MT477147	MT477147	Spirin et al. 2021
Megalocystidium leucoxanthum	HK9808	Sweden	AF506420	AF506420	Spirin et al. 2021
Mycobernardia incrustans	CBS:172.36	Canada	MH855759	MH867272	Vu et al. 2019
Mycobernardia incrustans	Duhem 3613	France	MW805860	MW805825	Ghobad-Nejhad et al. 2021
Neoaleurodiscus fujii	He2921	China	KU559357	KU574845	Dai et al. 2017
Neoaleurodiscus fujii	Wu0807-41	Japan	–	FJ799924	Dai et al. 2017
Peniophora halimi	CBS:864.84	France	MH861845	MH873533	Vu et al. 2019
Peniophora incarnata	CBS:398.50	France	MH856680	MH868197	Vu et al. 2019
Protodaedalea foliacea	Yuan 5691	China	JQ764666	JQ764644	Zhou and Dai 2013
Protodaedalea hispida	WD 548	Japan	AB871768	AB871749	Sotome et al. 2014
Punctularia atropurpurascens	UC 2022981	USA	KP814559	–	Knijn & Ferretti 2018
Punctularia atropurpurascens	WEI 17-662	China	MW570883	MW570888	Wei et al. 2022
Punctularia bambusicola	CLZhao 4133	China	MW559982	MW559984	Guan et al. 2021
Punctularia bambusicola	CLZhao 9098	China	MW559983	MW559985	Guan et al. 2021
Punctularia nigrodontea	CLZhao 30592*	China	PQ783829	PQ783839	Present study
Punctularia strigosozonata	AFTOL-ID 1248	–	DQ398958	AF518642	Wei et al. 2022
Punctularia strigosozonata	CBS:34534	–	MH855559	MH867064	Vu et al. 2019
Punctulariopsis efibulata	Burdsall 8824	USA	KR494276	KR494277	Wei et al. 2022
Punctulariopsis obducens	MG70	Ethiopia	HM046918	HM046933	Ghobad-Nejhad et al. 2010
Punctulariopsis subglobispora	FCUG 2535	Argentina	HM046917	HM046932	Guan et al. 2021
Russula blennia	569/BB08.066	Switzerland	MH545687	KU237556	Wu et al. 2020
Russula pseudociliata	545/BB08.061	Switzerland	MH545688	KU237537	Wu et al. 2020
Sclerotrema griseobrunneum	TN 2722	Canada	KX262144	KX262192	Malysheva and Spirin 2017
Sclerotrema griseobrunneum	VS 7674	Russia	KX262140	KX262188	Malysheva and Spirin 2017
Scytinostroma acystidiatum	Dai 24608	China	OQ689127	OQ629351	Zhang et al. 2023

Taxa	Voucher no.	Locality	GenBank accession no.		References
			ITS	nLSU	
Scytinostroma bambusinum	JXH 643	China	OR510627	PP660873	Ji et al. 2024
Sistotrema brinkmannii	236	Netherlands	JX535169	JX535170	Alvarenga and Gibertoni 2021
Stereodiscus pseudotrivialis	SPG6799	Argentina	OR506747	OR506751	Gorjón and Greslebin 2024
Stereodiscus pseudotrivialis	SPG6874	Argentina	OR506744	OR506746	Gorjón and Greslebin 2024
Stereum hirsutum	CBS:108532	Russia	MH862810	MH874407	Vu et al. 2019
Stereum sanguinolentum	CBS:529.50	Canada	MH856746	MH868268	Vu et al. 2019
Terrestriporia alba	Dai 18546	Malaysia	MT068562	MT068558	Wu et al. 2020
Terrestriporia alba	Dai 18547	Malaysia	MT068563	MT068559	Wu et al. 2020
Tremellochaete atlantica	URM90199	Brazil	MG594381	MG594383	Alvarenga et al. 2019
Tremellochaete cilliata	SP467241	Brazil	MK391523	MK391529	Alvarenga et al. 2019
Tremellochaete japonica	LE 303446	Russia	KX262110	KX262160	Malysheva and Spirin 2017
Vararia fissurata	CLZhao 8171	China	OQ025219	OR539503	Deng et al. 2024b
Vararia tropica	CBS:704.81	France	MH861447	MH873189	Vu et al. 2019
Vuilleminia comedens	AFTOL-ID 1247	–	DQ398959	AF518666	Wei et al. 2022
Vuilleminia coryli	MG136	Turkmenistan	JN387996	JN388005	Ghobad-Nejhad and Ginns 2012
Vuilleminia cystidiata	KUC20131022-26	Korea	KJ668433	KJ668285	Wei et al. 2022
Vuilleminia erastii	MG97	Canada	JN387998	JN388007	Ghobad-Nejhad and Ginns 2012
Vuilleminia macrospora	MG167	France	JX892940	JX892941	Ghobad-Nejhad and Duhem 2014
Vuilleminia nilsii	MG171	France	JX892947	JX892948	Ghobad-Nejhad and Duhem 2014
Vuilleminia pseudocystidiata	MG69	France	HM046888	HM046928	Ghobad-Nejhad et al. 2010
Waitea circinata	CBS:472.82	USA	MH861518	MH873265	Vu et al. 2019
Waitea guianensis	GUY13-110	Guiana	MW449090	MW449101	Wei et al. 2022
Xylobolus frustulatus	He2231	USA	KU881905	KU574825	Tian et al. 2018
Xylobolus subpileatus	FP-106735	USA	–	AY039309	Tian et al. 2018

assigned as an outgroup to root trees following the ITS+nLSU analysis (Fig. 2) (Deng et al. 2024b); (3) *Gloeophyllum abietinum* (Bull.) P. Karst. was assigned as an outgroup to root trees following the ITS+nLSU analysis (Fig. 3) (He et al. 2014); (4) *Sistotrema brinkmannii* (Bres.) J. Erikss. was assigned as an outgroup to root trees following the ITS+nLSU analysis (Fig. 4) (Alvarenga and Gibertoni 2021); (5) *Adustochaete punctata* J.H. Dong & C.L. Zhao were assigned as an outgroup to root trees following the ITS+nLSU analysis (Fig. 5) (Dong et al. 2024b).

Maximum parsimony (MP), maximum likelihood (ML), and Bayesian inference (BI) analyses were applied to the combined datasets following a previous study (Wu et al. 2022; Dong et al. 2024a), and the tree construction procedure was performed in PAUP* version 4.0b10 (Swofford 2002). All characters were equally weighted, and gaps were treated as missing data. Trees were inferred using the heuristic search option with TBR branch swapping and 1,000 random

sequence additions. Max trees were set to 5000, branches of zero length were collapsed, and all parsimonious trees were saved. Clade robustness was assessed using bootstrap (BT) analysis with 1000 replicates (Felsenstein 1985). Descriptive tree statistics, tree length (TL), consistency index (CI), retention index (RI), rescaled consistency index (RC), and homoplasy index (HI) were calculated for each maximum parsimonious tree generated. The multiple sequence alignment was also analyzed using maximum likelihood (ML) in RAxML-HPC2 (Miller et al. 2012). Branch support (BS) for ML analysis was determined by 1000 bootstrap replicates.

MrModeltest 2.3 (Nylander 2004) was used to determine the best-fit evolution model for each dataset for Bayesian inference (BI), which was performed using MrBayes 3.2.7a with a general time reversible model of DNA substitution and a gamma distribution rate variation across sites (Ronquist et al. 2012). Four Markov chains were run twice from a random starting tree for 0.4 million generations of the datasets (Fig. 1), 0.4 million generations of the datasets (Fig. 2), 1.6 million generations of the datasets (Fig. 3), 0.8 million generations of the datasets (Fig. 4), and for 0.6 million generations of the datasets (Fig. 5), and the tree was sampled every 1000 generations. The first one-fourth of all generations were discarded as burn-in. The majority rule consensus tree of all remaining trees was calculated. Branches were considered as significantly supported if they received a maximum likelihood bootstrap value (BS) ≥70%, maximum parsimony bootstrap value (BT) ≥50%, or Bayesian posterior probabilities (BPP) ≥0.95.

Results

The phylogeny of *Conferticium*

The datasets based on ITS+nLSU (Fig. 1) comprise sequences from 44 fungal specimens representing 39 species. The datasets had an aligned length of 2,270 characters, of which 1,183 characters are constant, 293 are variable and parsimony-uninformative, and 794 are parsimony-informative. Maximum parsimony analysis yielded 1 equally parsimonious tree (TL = 4447, CI = 0.4160, H = 0.5840, RI = 0.5275, RC = 0.2194). Bayesian analysis and ML analysis resulted in a similar topology as MP analysis with an average standard deviation of split frequencies of 0.008678 (BI), and the effective sample size (ESS) across the two runs is double the average ESS (avg ESS) = 144.5. The phylogenetic tree (Fig. 1) inferred from ITS+nLSU sequences revealed that the new species *Conferticium albocremeum* grouped into the genus *Conferticium* and clustered into the family Stereaceae (Russulales), in which it was retrieved as a sister to *C. heimii* (Boidin) Sheng H. Wu.

The datasets based on ITS+nLSU (Fig. 2) comprise sequences from 31 fungal specimens representing 23 species. The datasets had an aligned length of 2,136 characters, of which 1,456 characters are constant, 298 are variable and parsimony-uninformative, and 382 are parsimony-informative. Maximum parsimony analysis yielded 1 equally parsimonious tree (TL = 1491, CI = 0.6237, HI = 0.3763, RI = 0.5681, RC = 0.3544). Bayesian analysis and ML analysis resulted in a similar topology as MP analysis with an average standard deviation of split frequencies of 0.013157 (BI), and the effective sample size (ESS) across

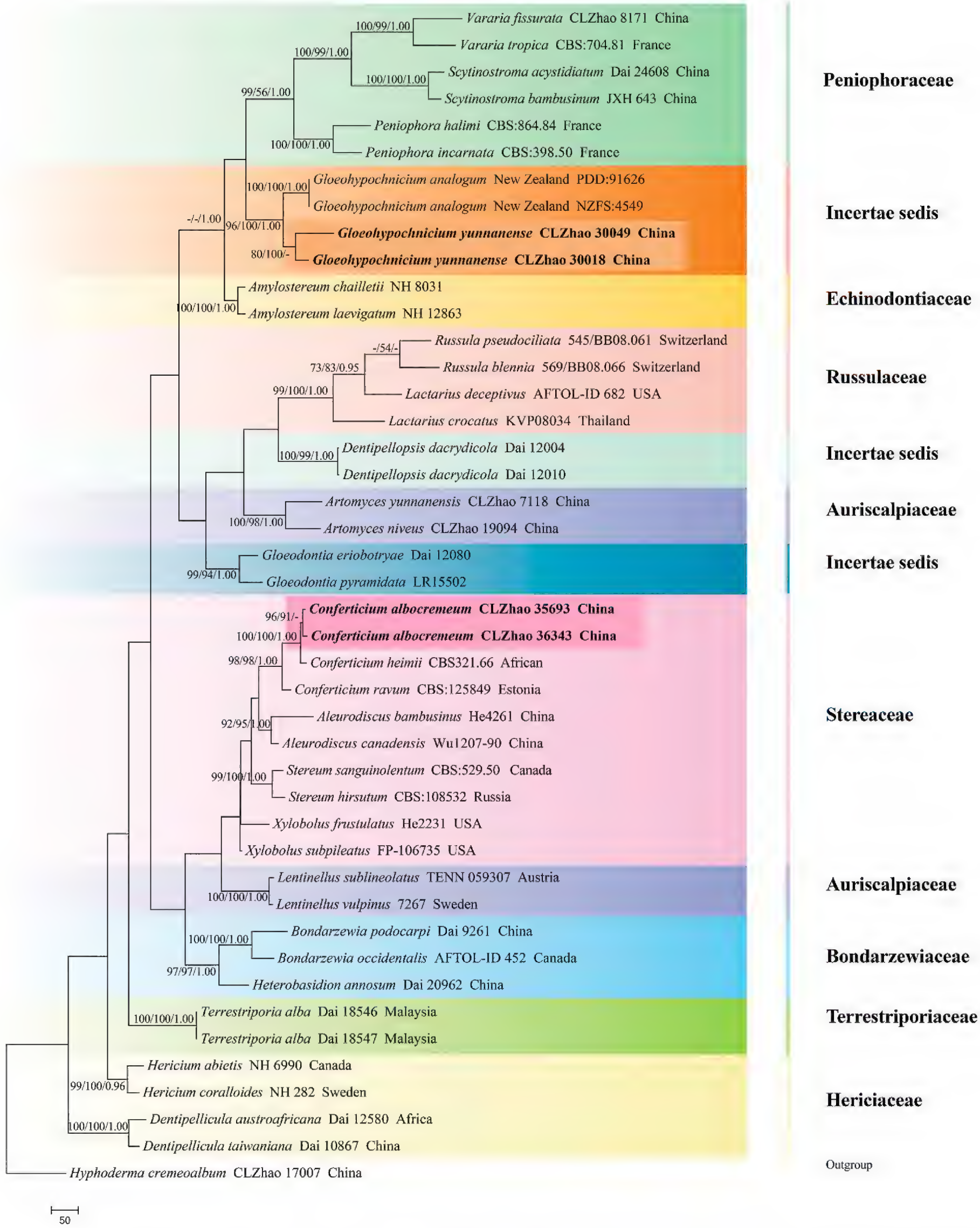

Figure 1. Maximum parsimony strict consensus tree illustrating the phylogeny of *Conferticium* and *Gloeohypochnicium* and related genera in the order Russulales, based on ITS+nLSU sequences; branches are labeled with maximum likelihood bootstrap value ≥ 70%, parsimony bootstrap value ≥ 50%, and Bayesian posterior probabilities ≥ 0.95.

the two runs is double the average ESS (avg ESS) = 265.5. The phylogenetic tree (Fig. 2) inferred from ITS+nLSU sequences revealed that *Conferticium albocremeum* grouped into the genus *Conferticium* and clustered into the family Stereaceae, in which it was closely related to *C. heimii*.

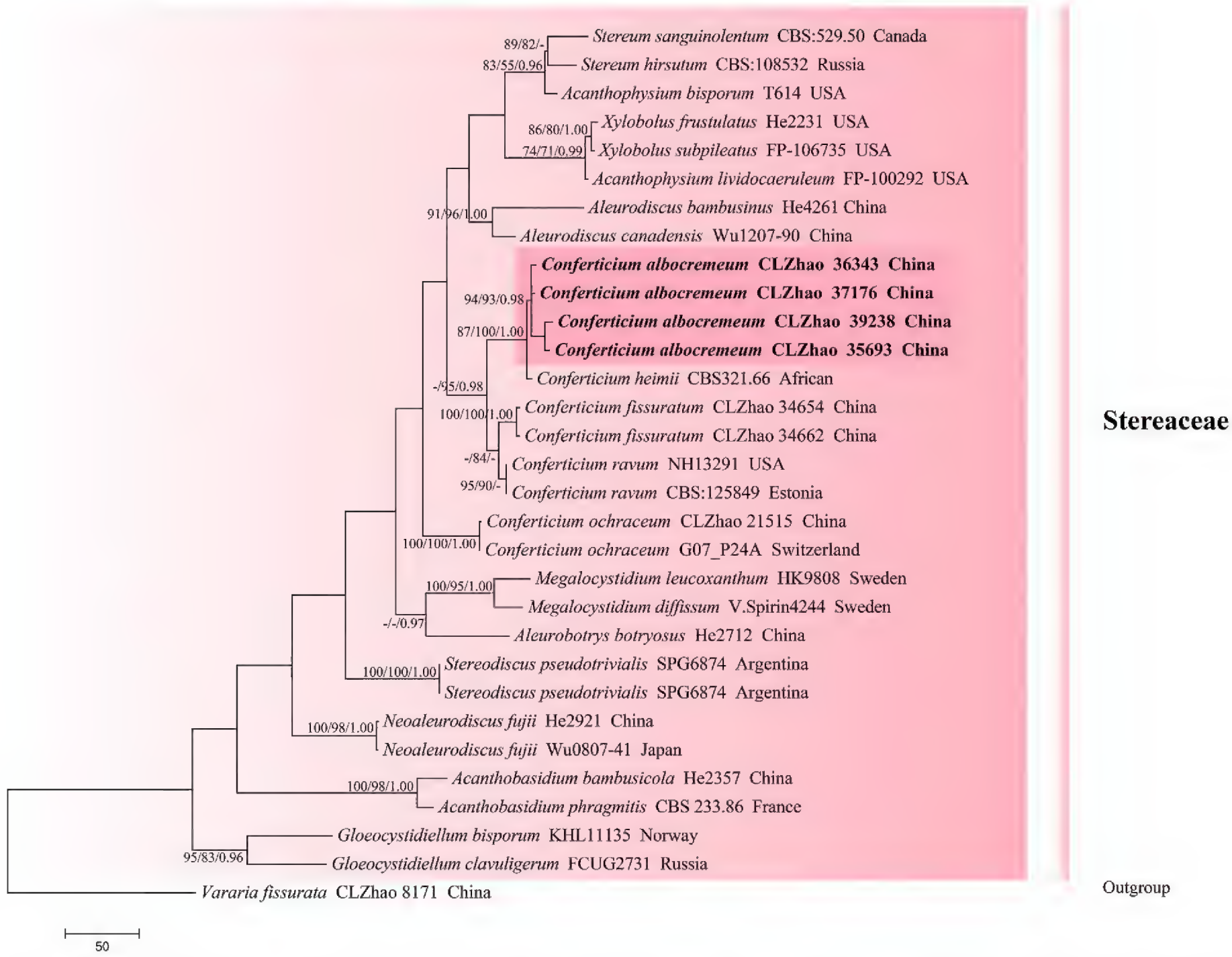

Figure 2. Maximum parsimony strict consensus tree illustrating the phylogeny of *Conferticium* and related genus in the family Stereaceae, based on ITS+nLSU sequences; branches are labeled with maximum likelihood bootstrap value ≥ 70%, parsimony bootstrap value ≥ 50%, and Bayesian posterior probabilities ≥ 0.95.

The phylogeny of *Dendrocorticiopsis*

The datasets based on ITS+nLSU (Fig. 3) comprise sequences from 44 fungal specimens representing 37 species. The datasets had an aligned length of 2,181 characters, of which 1,313 characters are constant, 232 are variable and parsimony-uninformative, and 736 are parsimony-informative. Maximum parsimony analysis yielded 1 equally parsimonious tree (TL = 3423, CI = 0.4368, HI = 0.5632, RI = 0.5695, RC = 0.2488). Bayesian analysis and ML analysis resulted in a similar topology as MP analysis with an average standard deviation of split frequencies of 0.013154 (BI), and the effective sample size (ESS) across the two runs is double the average ESS (avg ESS) = 658. The phylogenetic tree (Fig. 1) inferred from ITS+nLSU sequences revealed that the new species *Dendrocorticiopsis luteoalba* grouped into the genus *Dendrocorticiopsis* and clustered into the family Punctulariaceae (Corticiales), in which it was retrieved as a sister to *D. orientalis* Sheng H. Wu et al.

The phylogeny of *Eichleriella*

The datasets based on ITS+nLSU (Fig. 4) comprise sequences from 45 fungal specimens representing 43 species. The datasets had an aligned length of

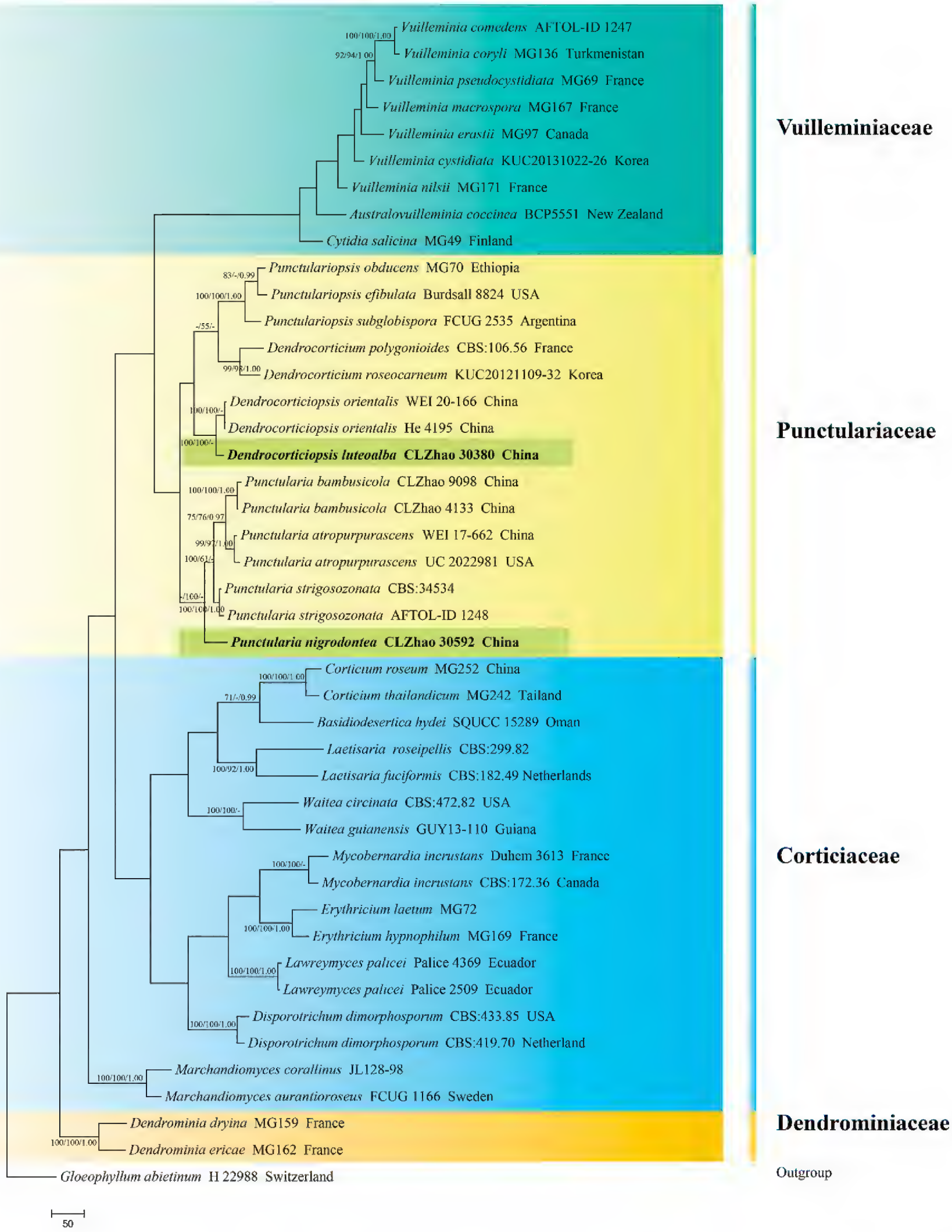

Figure 3. Maximum parsimony strict consensus tree illustrating the phylogeny of *Dendrocorticiopsis* and *Punctularia* and related genera in the order Corticiales, based on ITS+nLSU sequences; branches are labeled with maximum likelihood bootstrap value ≥ 70%, parsimony bootstrap value ≥ 50%, and Bayesian posterior probabilities ≥ 0.95.

2,104 characters, of which 1,516 characters are constant, 254 are variable and parsimony-uninformative, and 334 are parsimony-informative. Maximum parsimony analysis yielded 1 equally parsimonious tree (TL = 1783 CI = 0.4773, HI = 0.5227, RI = 0.5633, RC = 0.2688). Bayesian analysis and ML analysis resulted in a similar topology as MP analysis with an average standard deviation of split frequencies of 0.0024569 (BI), and the effective sample size (ESS) across the two runs is double the average ESS (avg ESS) = 361.5. The phylogenetic tree (Fig. 4)

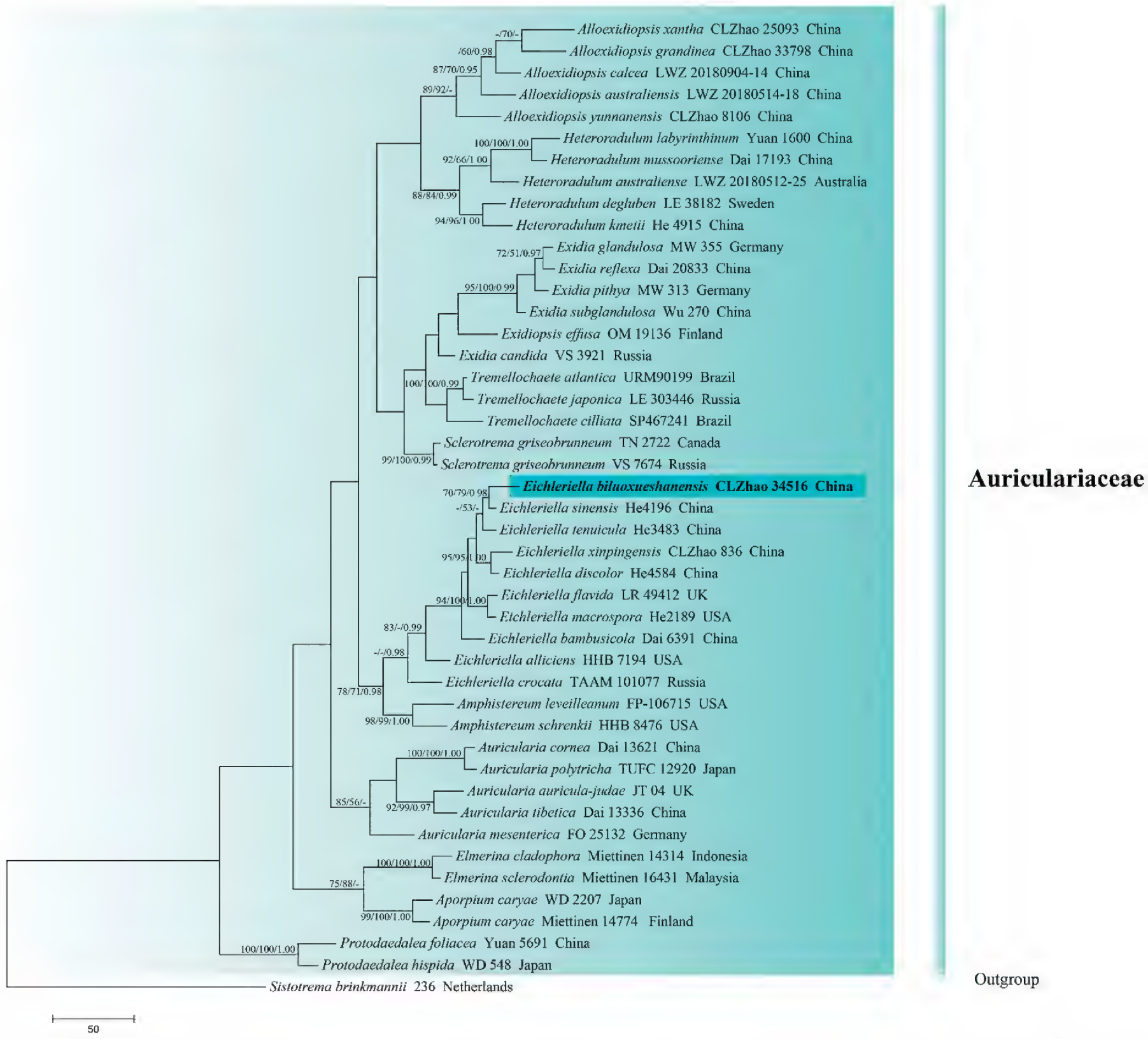
Alloexidiopsis xantha CLZhao 25093 China
Alloexidiopsis grandinea CLZhao 33798 China
Alloexidiopsis calcea LWZ 20180904-14 China
Alloexidiopsis australiensis LWZ 20180514-18 China
Alloexidiopsis yunnanensis CLZhao 8106 China
Heteroradulum labyrinthinum Yuan 1600 China
Heteroradulum mussooriense Dai 17193 China
Heteroradulum australiense LWZ 20180512-25 Australia
Heteroradulum degluben LE 38182 Sweden
Heteroradulum kmetii He 4915 China
Exidia glandulosa MW 355 Germany
Exidia reflexa Dai 20833 China
Exidia pithya MW 313 Germany
Exidia subglandulosa Wu 270 China
Exidiopsis effusa OM 19136 Finland
Exidia candida VS 3921 Russia
Tremellochaete atlantica URM90199 Brazil
Tremellochaete japonica LE 303446 Russia
Tremellochaete cilliata SP467241 Brazil
Sclerotrema griseobrunneum TN 2722 Canada
Sclerotrema griseobrunneum VS 7674 Russia
Eichleriella biluoxueshanensis CLZhao 34516 China
Eichleriella sinensis He4196 China
Eichleriella tenuicula He3483 China
Eichleriella xinpingensis CLZhao 836 China
Eichleriella discolor He4584 China
Eichleriella flavida LR 49412 UK
Eichleriella macrospora He2189 USA
Eichleriella bambusicola Dai 6391 China
Eichleriella alliciens HHB 7194 USA
Eichleriella crocata TAAM 101077 Russia
Amphistereum leveilleanum FP-106715 USA
Amphistereum schrenkii HHB 8476 USA
Auricularia cornea Dai 13621 China
Auricularia polytricha TUFC 12920 Japan
Auricularia auricula-judae JT 04 UK
Auricularia tibetica Dai 13336 China
Auricularia mesenterica FO 25132 Germany
Elmerina cladophora Miettinen 14314 Indonesia
Elmerina sclerodontia Miettinen 16431 Malaysia
Aporpium caryae WD 2207 Japan
Aporpium caryae Miettinen 14774 Finland
Protodaedalea foliacea Yuan 5691 China
Protodaedalea hispida WD 548 Japan
Sistotrema brinkmannii 236 Netherlands
50
Auriculariaceae
Outgroup

Figure 4. Maximum parsimony strict consensus tree illustrating the phylogeny of *Eichleriella* and related genera in the family Auriculariaceae, based on ITS+nLSU sequences; branches are labeled with maximum likelihood bootstrap value ≥ 70%, parsimony bootstrap value ≥ 50%, and Bayesian posterior probabilities ≥ 0.95.

inferred from ITS+nLSU sequences revealed that *Eichleriella biluoxueshanensis* grouped into the genus *Eichleriella* and clustered into the family Auriculariaceae, in which it was retrieved as a sister to *E. sinensis* (Teng) S.H. He & Nakasone.

The datasets based on ITS+nLSU (Fig. 5) comprise sequences from 31 fungal specimens representing 24 species. The datasets had an aligned length of 1,905 characters, of which 1,687 characters are constant, 101 are variable and parsimony-uninformative, and 117 are parsimony-informative. Maximum parsimony analysis yielded 1 equally parsimonious tree (TL = 402, CI = 0.6542, HI = 0.3458, RI = 0.7495, RC = 0.4094). Bayesian analysis and ML analysis resulted in a similar topology as MP analysis with an average standard deviation of split frequencies of 0.009368 (BI), and the effective sample size (ESS) across the two runs is double the average ESS (avg ESS) = 264.5. The phylogenetic tree (Fig. 5) inferred from ITS+nLSU sequences revealed that *Eichleriella biluoxueshanensis* grouped into the genus *Eichleriella*, in which it was grouped with the clade comprising *E. sinensis* (Teng) S.H. He & Nakasone.

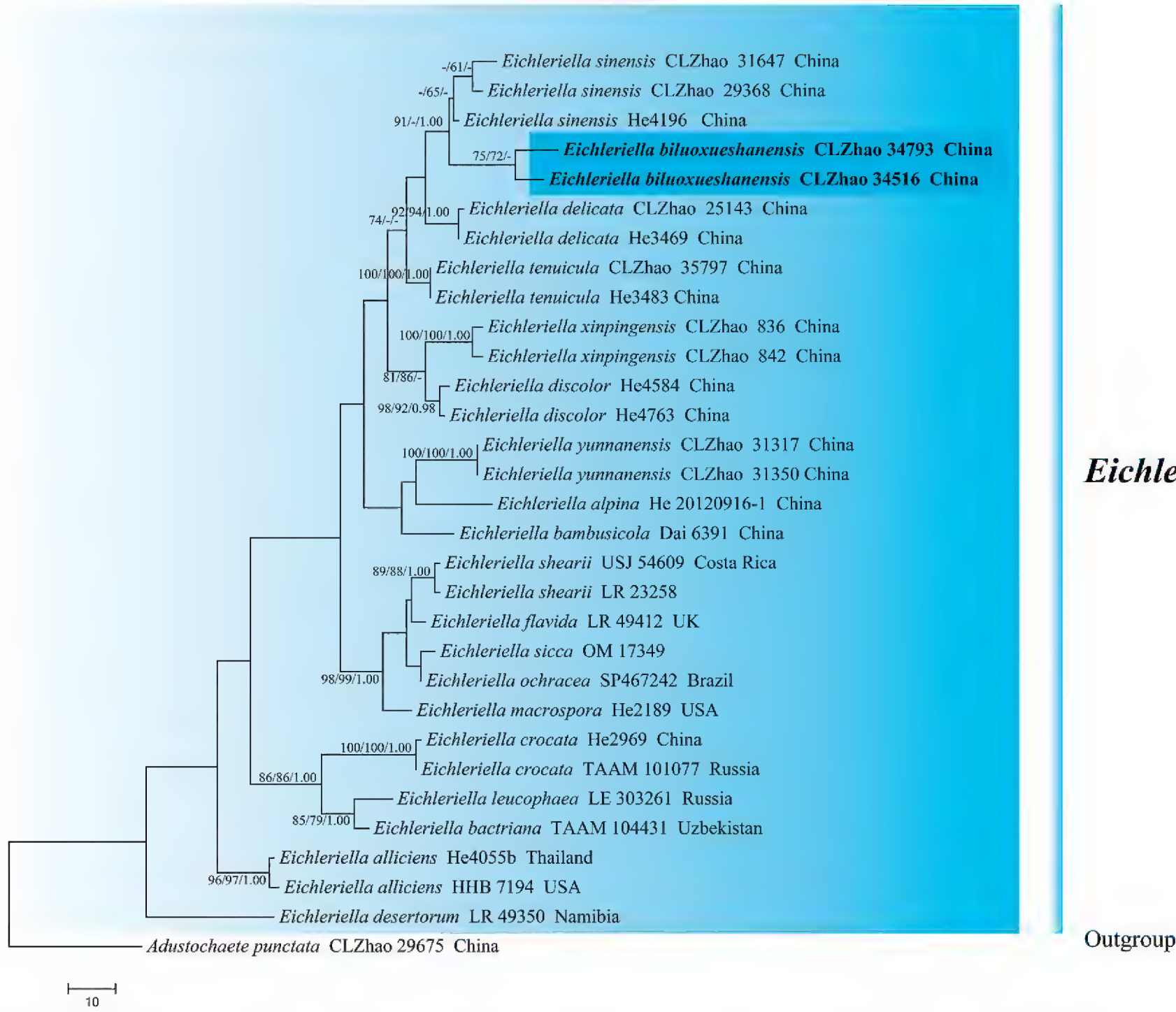

Figure 5. Maximum parsimony strict consensus tree illustrating the phylogeny of *Eichleriella* and related species in the genus *Eichleriella*, based on ITS+nLSU sequences; branches are labeled with maximum likelihood bootstrap value ≥ 70%, parsimony bootstrap value ≥ 50%, and Bayesian posterior probabilities ≥ 0.95.

The phylogeny of *Gloeohypochnicium*

The datasets based on ITS+nLSU (Fig. 1) comprise sequences from 44 fungal specimens representing 39 species. The datasets had an aligned length of 2,270 characters, of which 1,183 characters are constant, 293 are variable and parsimony-uninformative, and 794 are parsimony-informative. Maximum parsimony analysis yielded 1 equally parsimonious tree (TL = 4447, CI = 0.4160, HI = 0.5840, RI = 0.5275, RC = 0.2194). Bayesian analysis and ML analysis resulted in a similar topology as MP analysis with an average standard deviation of split frequencies of 0.008678 (BI), and the effective sample size (ESS) across the two runs is double the average ESS (avg ESS) = 144.5. The phylogenetic tree (Fig. 1) inferred from ITS+nLSU sequences revealed that *Gloeohypochnicium yunnanense* grouped into the genus *Gloeohypochnicium* and clustered into the order Russulales, in which it was closely related to *G. analogum* (Bourdot & Galzin) Hjortstam.

The phylogeny of *Punctularia*

The datasets based on ITS+nLSU (Fig. 3) comprise sequences from 44 fungal specimens representing 37 species. The datasets had an aligned length of

2,181 characters, of which 1,313 characters are constant, 232 are variable and parsimony-uninformative, and 736 are parsimony-informative. Maximum parsimony analysis yielded 1 equally parsimonious tree (TL = 3423, CI = 0.4368, HI = 0.5632, RI = 0.5695, RC = 0.2488). Bayesian analysis and ML analysis resulted in a similar topology as MP analysis with an average standard deviation of split frequencies of 0.013154 (BI), and the effective sample size (ESS) across the two runs is double the average ESS (avg ESS) = 658. The phylogenetic tree (Fig. 1) inferred from ITS+nLSU sequences revealed that *Punctularia nigrodontea* grouped into the genus *Punctularia* and clustered into the family Punctulariaceae (Corticiales), in which it was grouped with the clade comprising *P. atropurpurascens* (Berk. & Broome) Petch, *P. bambusicola* C.L. Zhao and *P. strigosozonata* (Schwein.) P.H.B. Talbot.

Taxonomy

Conferticium albocremeum **L. Wang & C.L. Zhao, sp. nov.**

MycoBank No: 856958

Figs 6–8

Typification. China. Yunnan Province • Xishuangbanna, Wild Elephant Valley, GPS coordinates: 22°10'N, 100°51'E, altitude: 900 m asl., on the fallen angiosperm branch, leg. C.L. Zhao, 25 January 2024 CLZhao 35693 (SWFC!).

Etymology. *Albocremeum* (Lat.) refers to the new species having white to cream hymenophore.

Basidiomata. Annual, resupinate, closely adnate, membranaceous, without odor or taste when fresh, up to 10 cm long, 2 cm wide, and 700 μm thick. Hymenophore smooth, white (60) to cream (4A2/3) when fresh, cream (4A2/3) upon drying. Sterile margin narrow, cream (4A2/3), up to 1 mm.

Hyphal system. Monomitic; generative hyphae with simple-septa, colorless, thin-walled, smooth, rarely branched, interwoven, IKI+, CB–, 2–3 μm in diameter; tissues unchanged in KOH.

Hymenium. Gloeocystidia subclavate, flexuous, colorless, mostly constricted in the middle, thin-walled, smooth, 33–47.5 × 5–8 μm. Basidia subcylindrical to subclavate, slightly flexuous, with a basal simple septum and four sterigmata, 22–36 × 4.5–7 μm; basidioles numerous, in shape similar to basidia.

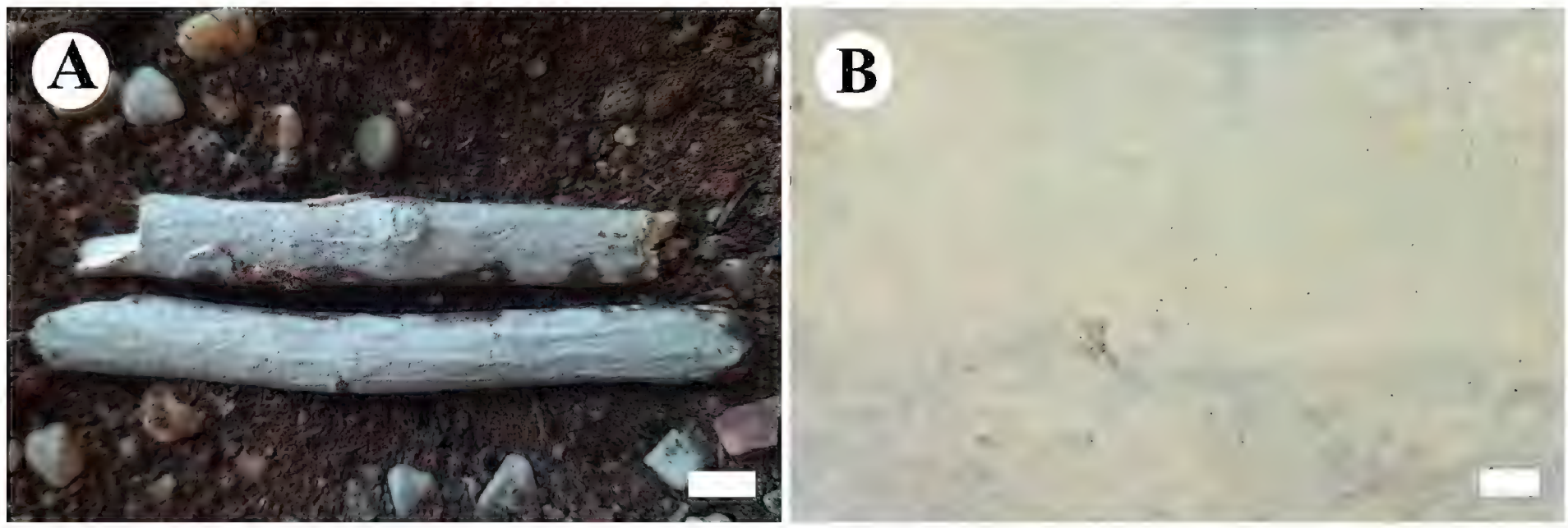

Figure 6. Basidiomata of *Conferticium albocremeum* (holotype CLZhao 35693). Scale bars: 1 cm (**A**); 1 mm (**B**).

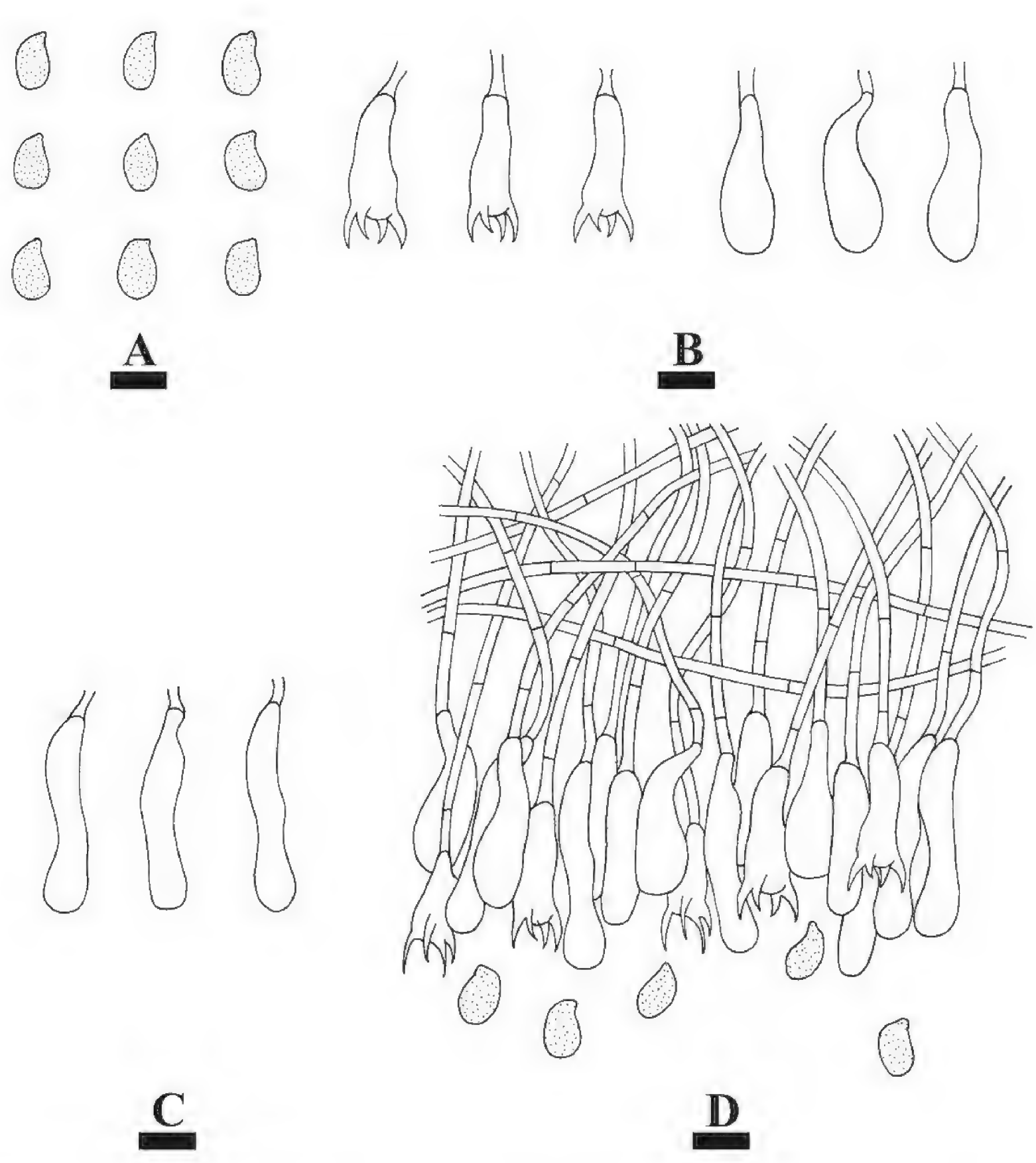

Figure 7. Microscopic structures of *Conferticium albocremeum* (holotype CLZhao 35693): basidiospores (**A**); basidia and basidioles (**B**); gloeocystidia (**C**); a section of the hymenium (**D**). Scale bars: 10 μm (**A–D**).

Spores. Basidiospores ellipsoid with a distinct apiculus, colorless, thin-walled, finely verrucose but appearing smooth by light microscope, IKI+, CB–, 9–11 × 5–7 μm, L = 9.82 μm, W = 5.84 μm, Q = 1.36–1.68 (n = 90/3).

Additional specimens examined (paratypes). China. Yunnan Province • Dehong, Mang City, Mengga Town, Tongbiguan Provincial Nature Reserve, GPS coordinates: 24°46'N, 97°34'E, altitude: 1300 m asl., on the fallen angiosperm branch, leg. C.L. Zhao, 29 June 2024, CLZhao 36343 • Dehong, Yingjiang County, Tongbiguan Provincial Nature Reserve, GPS coordinates: 25°50'N, 97°36'E, altitude: 1000 m asl., on the fallen angiosperm branch, leg. C.L. Zhao, 2 July 2024, CLZhao 37176 • Tengchong, Tuantian Town, Gaoligongshan National Nature Reserve, GPS coordinates: 25°27'N, 98°46'E, altitude: 2500 m asl., on the fallen angiosperm branch, leg. C.L. Zhao, 7 July 2024, CLZhao 39283 (SWFC!).

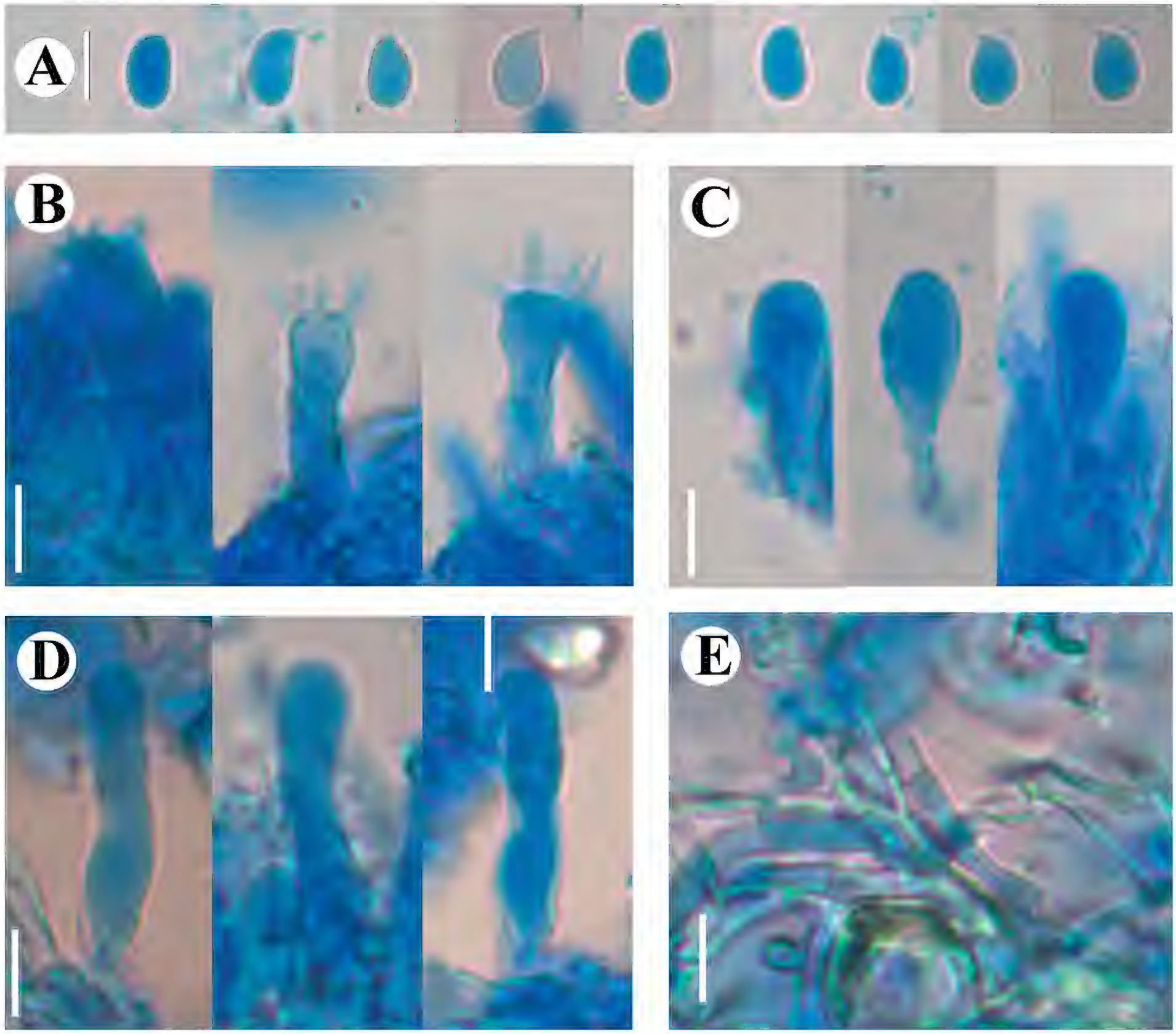

Figure 8. Sections of hymenium of *Conferticium albocremeum* (holotype CLZhao 35693): basidiospores (**A**); basidia (**B**); basidioles (**C**); gloeocystidia (**D**); a section of the generative hyphae (**E**). Scale bars: 10 μm (**A–E**); 10 × 100.

Dendrocorticiopsis luteoalba **L. Wang & C.L. Zhao, sp. nov.**

MycoBank No: 856959

Figs 9–11

Typification. China. Yunnan Province • Dehong, Yingjiang County, Tongbiguan Provincial Nature Reserve, GPS coordinates: 25°50'N, 97°36'E, altitude: 1000 m asl., on the fallen angiosperm branch, leg. C.L. Zhao, 19 July 2023, CLZhao 30380 (SWFC!).

Etymology. *Luteoalba* (Lat.) refers to the new species having a white to buff hymenophore.

Basidiomata. Annual, resupinate, closely adnate, membranaceous, without odor or taste when fresh, up to 6 cm long, 2 cm wide, and 300 μm thick. Hymenophore smooth, white (60) when fresh, white (60) to buff (4A4) upon drying. Sterile margin narrow, white (60) to buff (4A4), up to 1 mm.

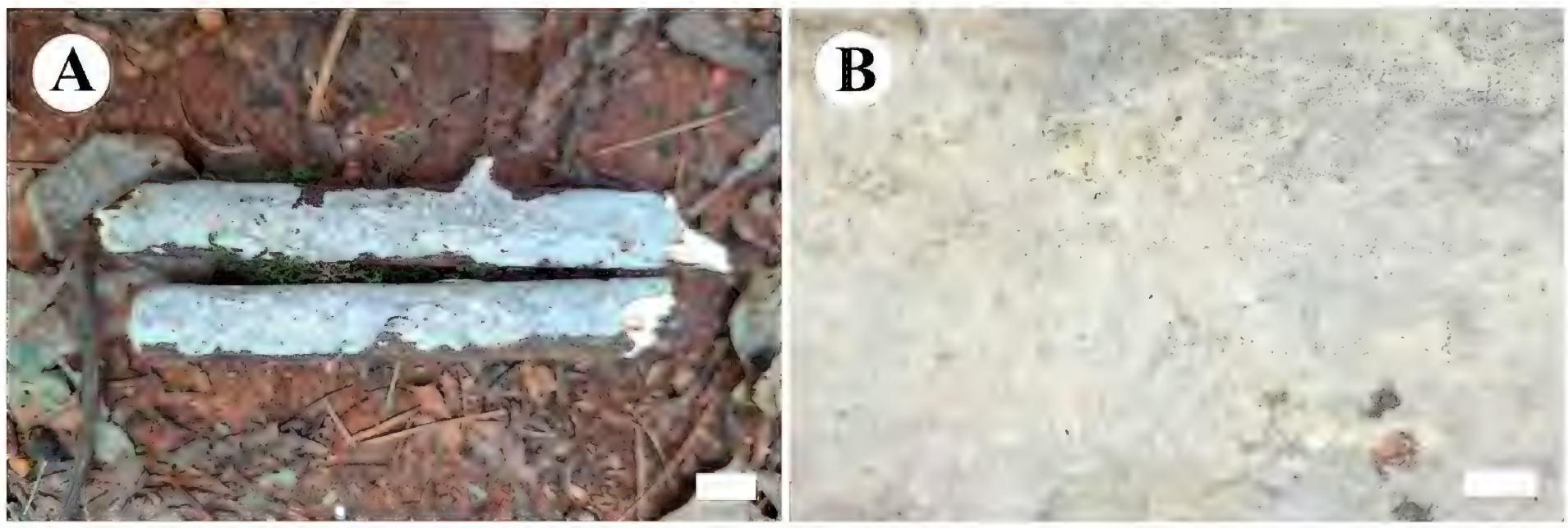

Figure 9. Basidiomata of *Dendrocorticiopsis luteoalba* (holotype CLZhao 30380). Scale bars: 1 cm (**A**); 1 mm (**B**).

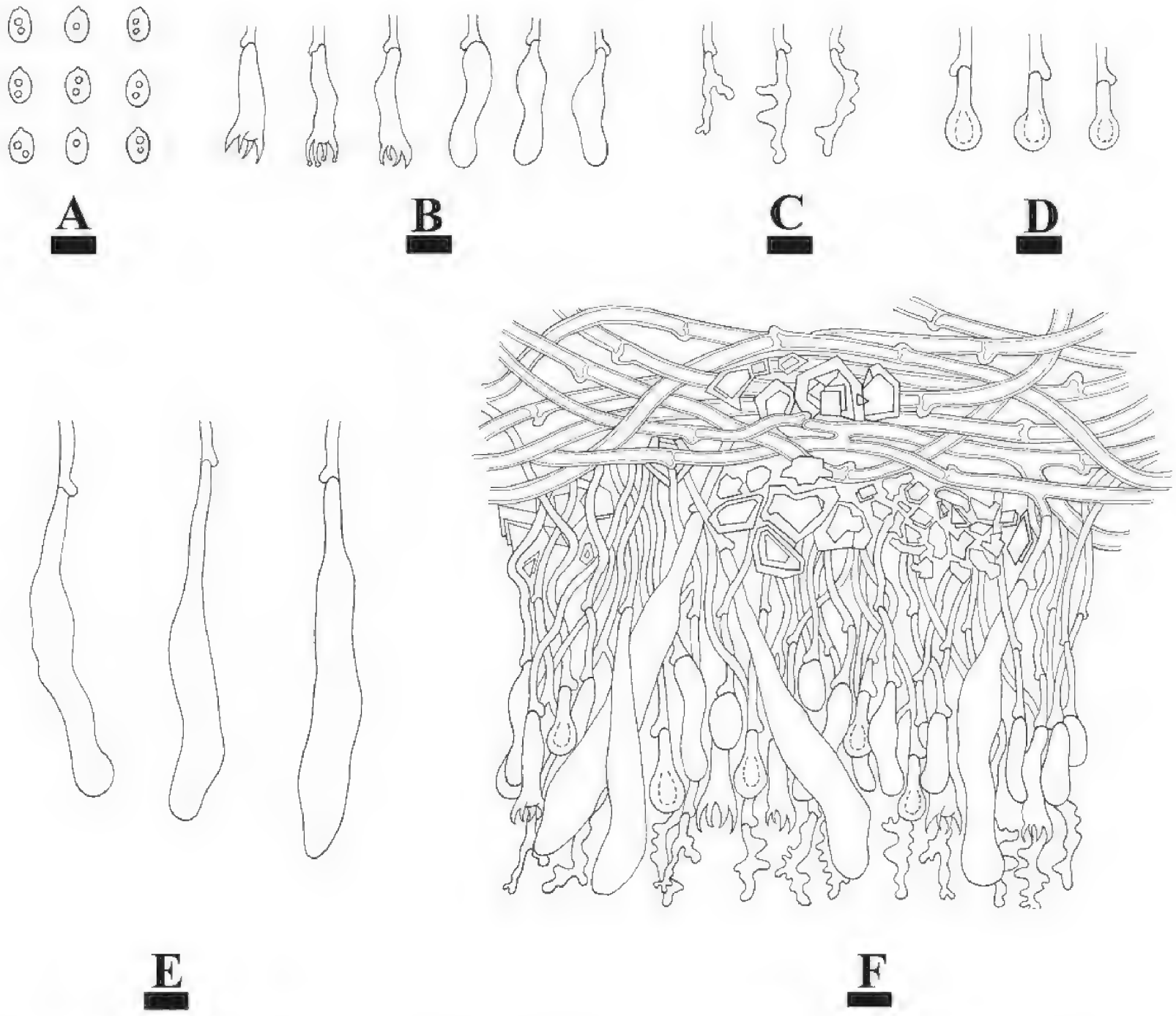

Figure 10. Microscopic structures of *Dendrocorticiopsis luteoalba* (holotype CLZhao 30380): basidiospores (**A**); basidia and basidioles (**B**); dendrohyphidia (**C**); cystidia (**D**); gloeocystidia (**E**); a section of the hymenium (**F**). Scale bars: 10 μm (**A–F**).

Hyphal system. Monomitic; generative hyphae with clamp connections, colorless, thin- to slightly thick-walled, smooth, branched, interwoven, usually with crystal masses, IKI–, CB–, 2.5–4 μm in diameter; tissues unchanged in KOH.

Hymenium. Cystidia are of two types: (1) capitate, apically with resinous materials, gradually dissolving in KOH, colorless, thin-walled, smooth, 8.5–14 ×

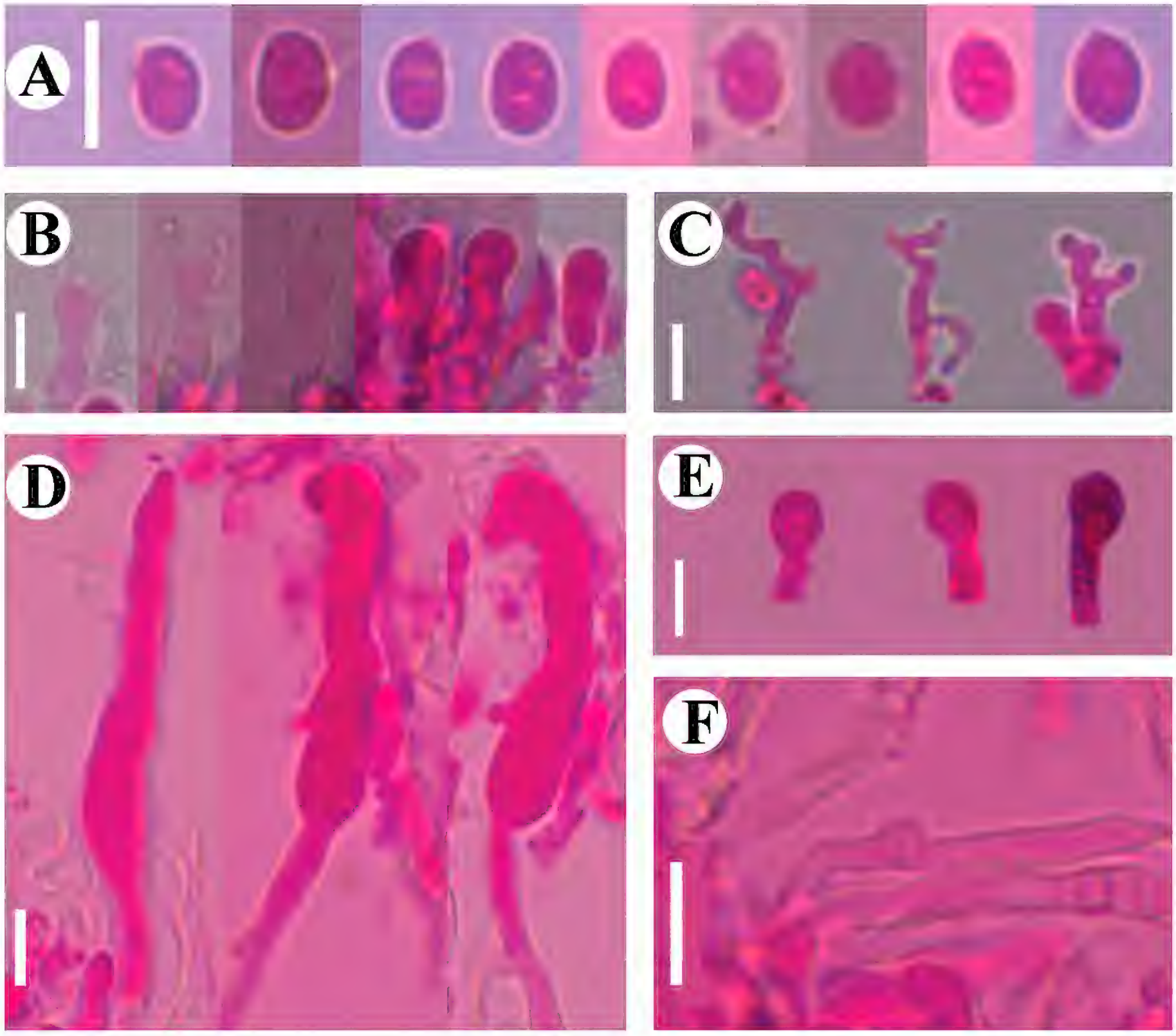

Figure 11. Sections of hymenium of *Dendrocorticiopsis luteoalba* (holotype CLZhao 30380): basidiospores (**A**); basidia and basidioles (**B**); dendrohyphidia (**C**); gloeocystidia (**D**); cystidia (**E**); a section of generative hyphae (**F**). Scale bars: 10 μm (**A–F**); 10 × 100.

6.5–8.5 μm; (2) gloeocystidia, clavate to subulate, slightly flexuous, colorless, thin-walled, smooth, 68.5–90 × 8–10 μm. Dendrohyphidia numerous, thick-walled toward base, colorless, 16–19 × 2.5–3.5 μm. Basidia subclavate to clavate, flexuous, with a basal clamp connection and four sterigmata, 15.5–28.5 × 4–5.5 μm; basidioles numerous, in shape similar to basidia.

Spores. Basidiospores ellipsoid, colorless, thin-walled, smooth, IKI–, CB–, (6.5–)7–8 × (4–)4.5–5.5 μm, L = 7.29 μm, W = 4.97μm, Q = 1.47 (n = 30/1).

Eichleriella biluoxueshanensis **L. Wang & C.L. Zhao, sp. nov.**

MycoBank No: 856960

Figs 12–14

Typification. China. Yunnan Province • Diqing, Weixi County, Weideng, Songpo, GPS coordinates: 27°05'N, 99°13'E, altitude: 1400 m asl., on the fallen angiosperm branch, leg. C.L., 13 November 2023, CLZhao 34516 (SWFC!).

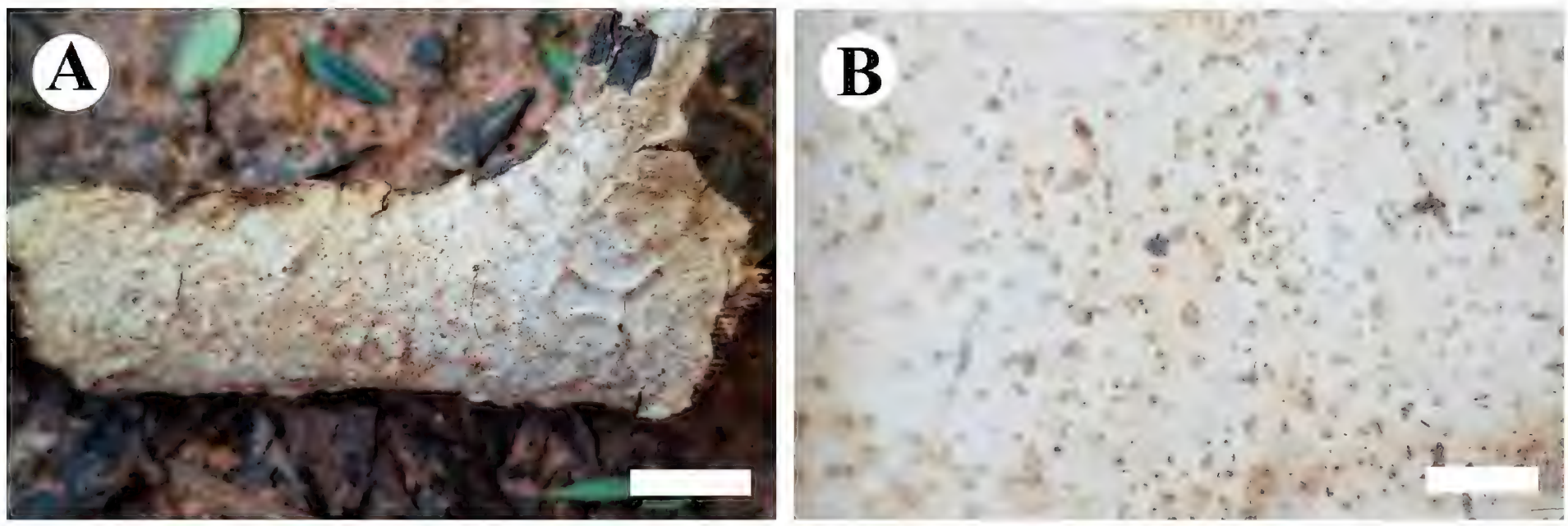

Figure 12. Basidiomata of *Eichleriella biluoxueshanensis* (holotype CLZhao 34516). Scale bars: 1 cm (**A**); 1 mm (**B**).

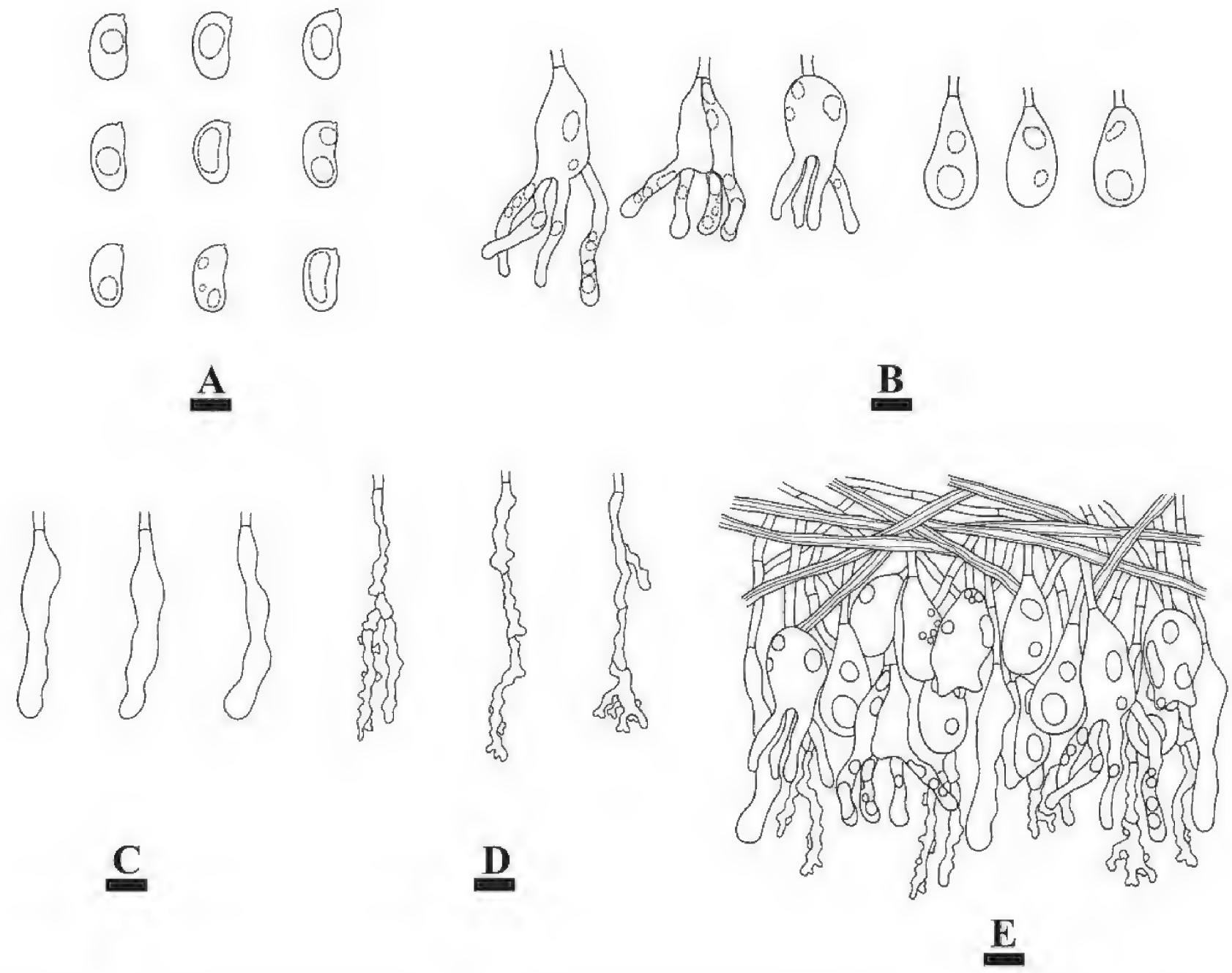

Figure 13. Microscopic structures of *Eichleriella biluoxueshanensis* (holotype CLZhao 34516): basidiospores (**A**); basidia and basidioles (**B**); cystidia (**C**); hyphidia (**D**); a section of the hymenium (**E**). Scale bars: 10 μm (**A–E**).

Etymology. *Biluoxueshanensis* (Lat.) refers to the locality (Biluoxueshan) of the holotype specimen.

Basidiomata. Annual, resupinate, closely adnate, coriaceous, without odor or taste when fresh, up to 8 cm long, 2 cm wide, and 700 μm thick. Hymenophore grandinioid, cream (4A2/3) to buff (4A4) when fresh, buff (4A4) to cinnamon-buff (4/5B4) upon drying. Sterile margin narrow, white (60) to cream (4A2/3), up to 1 mm.

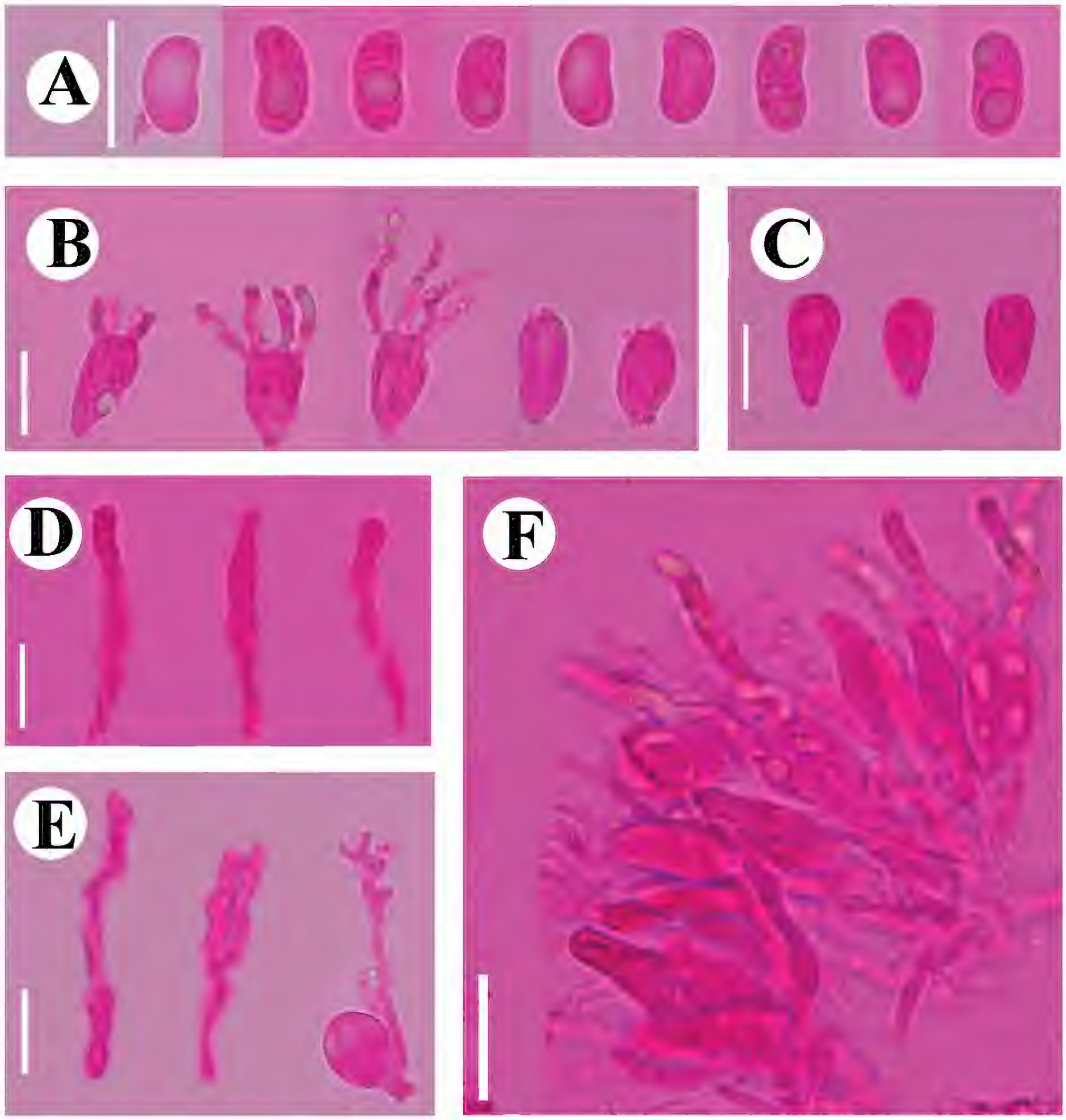

Figure 14. Sections of hymenium of *Eichleriella biluoxueshanensis* (holotype CLZhao 34516): basidiospores (**A**); basidia (**B**); basidioles (**C**); cystidia (**D**); hyphidia (**E**); a section of the hymenium (**F**). Scale bars: 10 μm (**A–F**); 10 × 100.

Hyphal system. Dimitic; generative hyphae simple-septate, colorless, thin-walled, smooth, rarely branched, interwoven, 3–4 μm in diameter; skeletal hyphae distinctly thick-walled, smooth, unbranched, interwoven, IKI–, CB–, 3–4 μm in diameter; tissues unchanged in KOH.

Hymenium. Cystidia subclavate, flexuous, colorless, thin-walled, smooth, 40–45.5 × 6–9.5 μm. Basidia narrowly ovoid to ellipsoid, longitudinally septate, four-celled, 21–29 × 11.5–15 μm; basidioles numerous, in shape similar to basidia but smaller. Hyphidia arising from generative hyphae, nodulose, branched, colorless, thin-walled, 58–72.5 × 2.5–4 μm in diameter.

Spores. Basidiospores allantoid, colorless, thin-walled, smooth, usually with one or more oil drops, IKI–, CB–, (12–)13.5–17.5(–18) × (6.5–)7–9(–9.5) μm, L = 15.57 μm, W = 7.99 μm, Q = 1.95–2.06 (n = 60/2).

Additional specimen examined (paratype). CHINA. Yunnan Province • Diqing, Weixi County, Zhonglu, Lagaluo, GPS coordinates: 27°9'N, 99°8'E, altitude: 1710 m asl., on the fallen angiosperm branch, leg. C.L. Zhao, 10 October 2023, CLZhao 34793 (SWFC!).

***Gloeohypochnicium yunnanense* L. Wang & C.L. Zhao, sp. nov.**

MycoBank No: 856961

Figs 15–17

Typification. CHINA. Yunnan Province • Dehong, Yingjiang County, Tongbiguan Provincial Nature Reserve, GPS coordinates: 25°50'N, 97°36'E, altitude: 1000 m asl., on the dead bamboo, leg. C.L. Zhao, 18 July 2023, CLZhao 30049 (SWFC!).

Etymology. *Yunnanense* (Lat.) refers to the locality "Yunnan Province" of the holotype specimen.

Basidiomata. Annual, resupinate, closely adnate, coriaceous, without odor or taste when fresh, up to 5 cm long, 3 cm wide, and 600 μm thick. Hymenophore smooth, slightly buff (4A4) when fresh, buff (4A4) to cream (4A2/3) upon drying. Sterile margin narrow, white (60) to buff (4A4), up to 1 mm.

Hyphal system. Monomitic; generative hyphae with clamp connections, colorless, thick-walled, smooth, branched, interwoven, 1.5–4 μm in diameter; IKI–, CB–, tissues unchanged in KOH.

Hymenium. Cystidia subcylindrical to subulate, flexuous, thin-walled, encrusted with whitish to yellowish crystals, 75–115.5 × 11.5–15 μm. Basidia subcylindrical to clavate, slightly flexuous, a basal clamp connection and four sterigmata, 55.5–70 × 9.5–11 μm; basidioles numerous, in shape similar to basidia but smaller.

Spores. Basidiospores globose, colorless, thick-walled, warted, IKI–, CB–, (9.5–)10–12 × (9.5–)10–11.5 μm, L = 10.91 μm, W = 10.45 μm, Q = 1.04–1.05 (n = 60/2).

Additional specimen examined (paratype). CHINA. Yunnan Province • Dehong, Yingjiang County, Tongbiguan Provincial Nature Reserve, GPS coordinates: 27°52'N, 97°38'E, altitude: 1000 m asl., on dead bamboo, leg. C.L. Zhao, 18 July 2023, CLZhao 30018 (SWFC!).

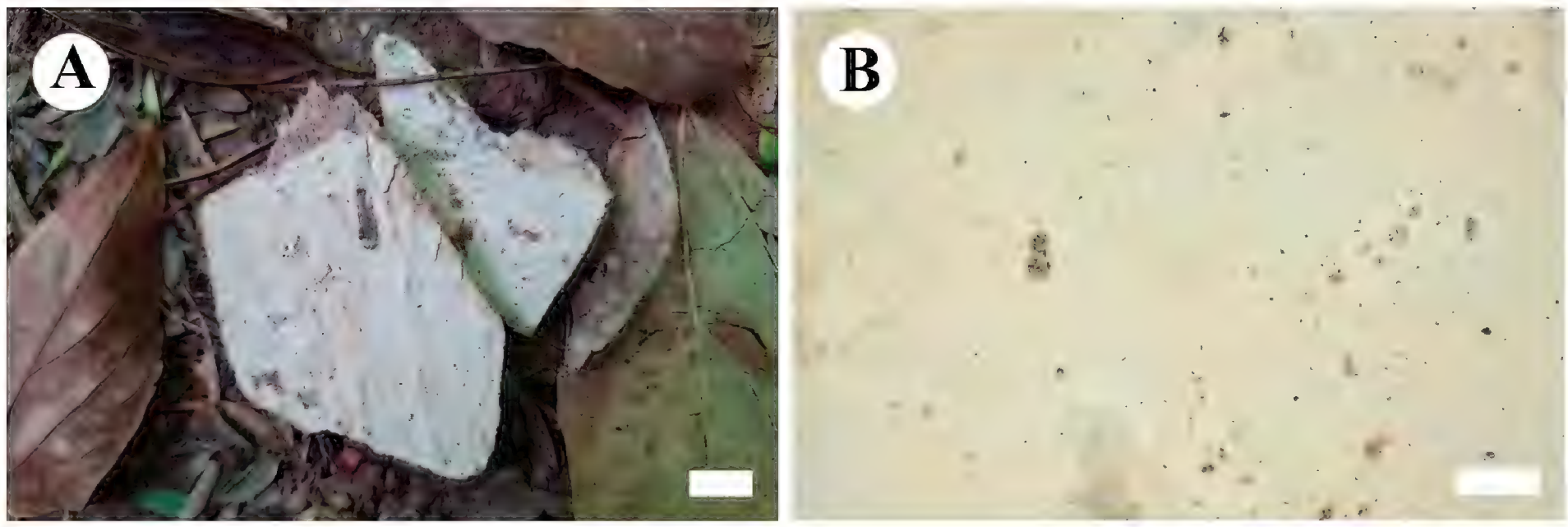

Figure 15. Basidiomata of *Gloeohypochnicium yunnanense* (holotype CLZhao 30049). Scale bars: 1 cm (**A**); 1 mm (**B**).

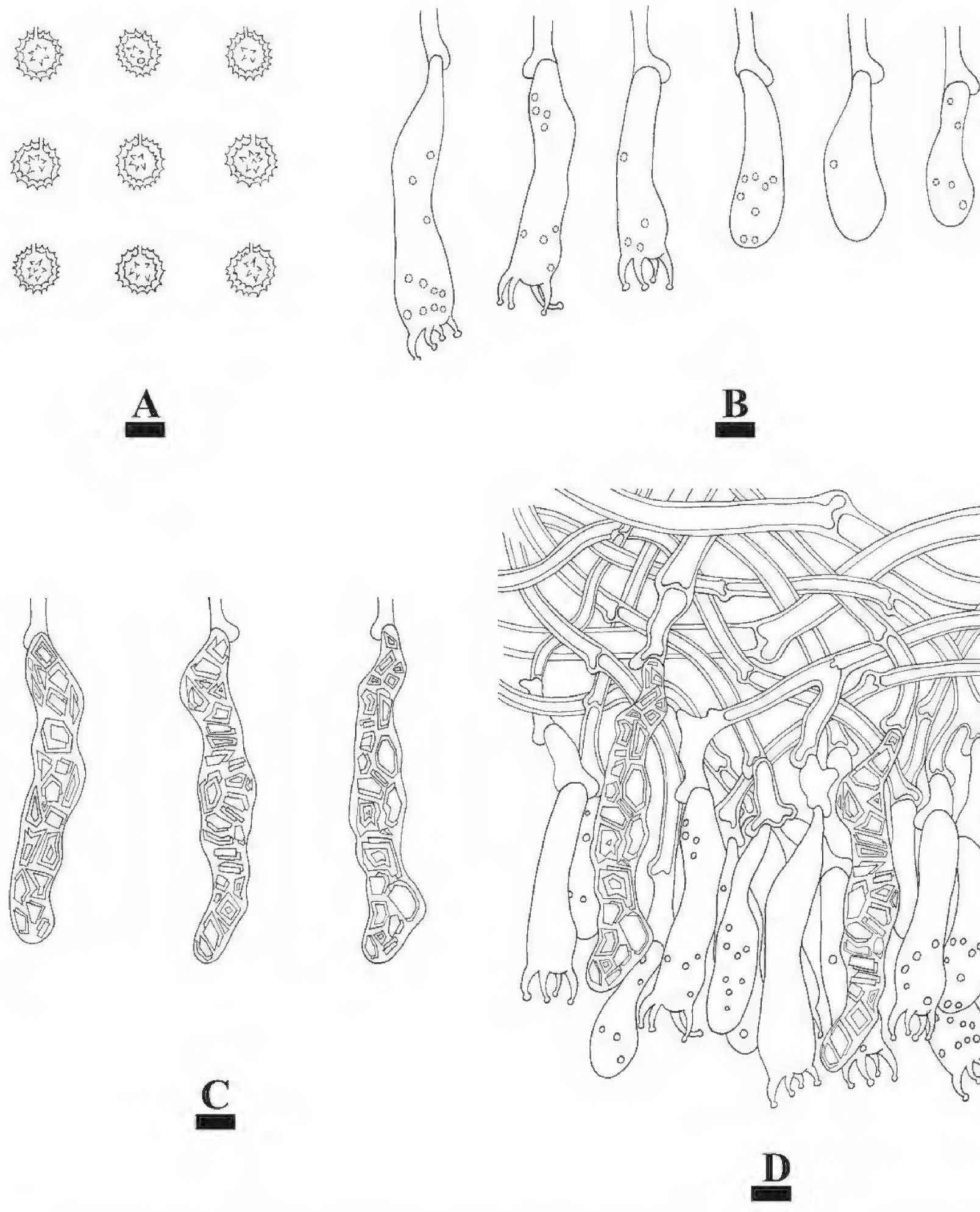

Figure 16. Microscopic structures of *Gloeohypochnicium yunnanense* (holotype CLZhao 30049): basidiospores (**A**); basidia and basidioles (**B**); cystidia (**C**); a section of the hymenium (**D**). Scale bars: 10 μm (**A–D**).

Punctularia nigrodontea **L. Wang & C.L. Zhao, sp. nov.**

MycoBank No: 856962

Figs 18–20

Typification. China. Yunnan Province • Dehong, Yingjiang County, Tongbiguan Provincial Nature Reserve, GPS coordinates: 25°50'N, 97°36'E, altitude: 1000 m asl., on the angiosperm trunk, leg. C.L. Zhao, 20 July 2023, CLZhao 30592 (SWFC!).

Etymology. *Nigrodontea* (Lat.) refers to the new species having black basidiomata.

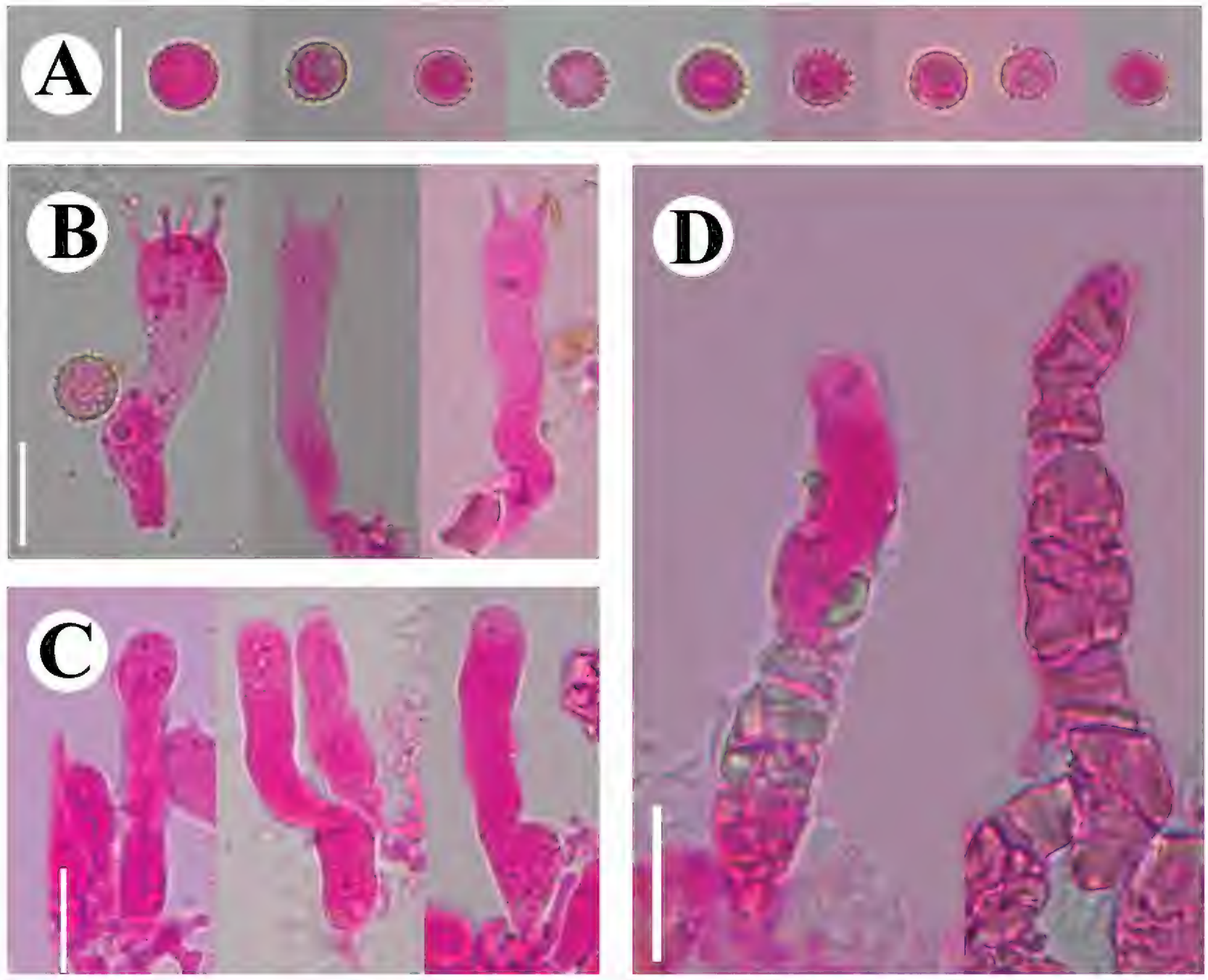

Figure 17. Sections of hymenium of *Gloeohypochnicium yunnanense* (holotype CLZhao 30049): basidiospores (**A**); basidia (**B**); basidioles (**C**); gloeocystidia (**D**). Scale bars: 20 μm (**A–D**); 10 × 100.

Figure 18. Basidiomata of *Punctularia nigrodontea* (holotype CLZhao 30592). Scale bars: 1 cm (**A, B**); 1 mm (**C, D**).

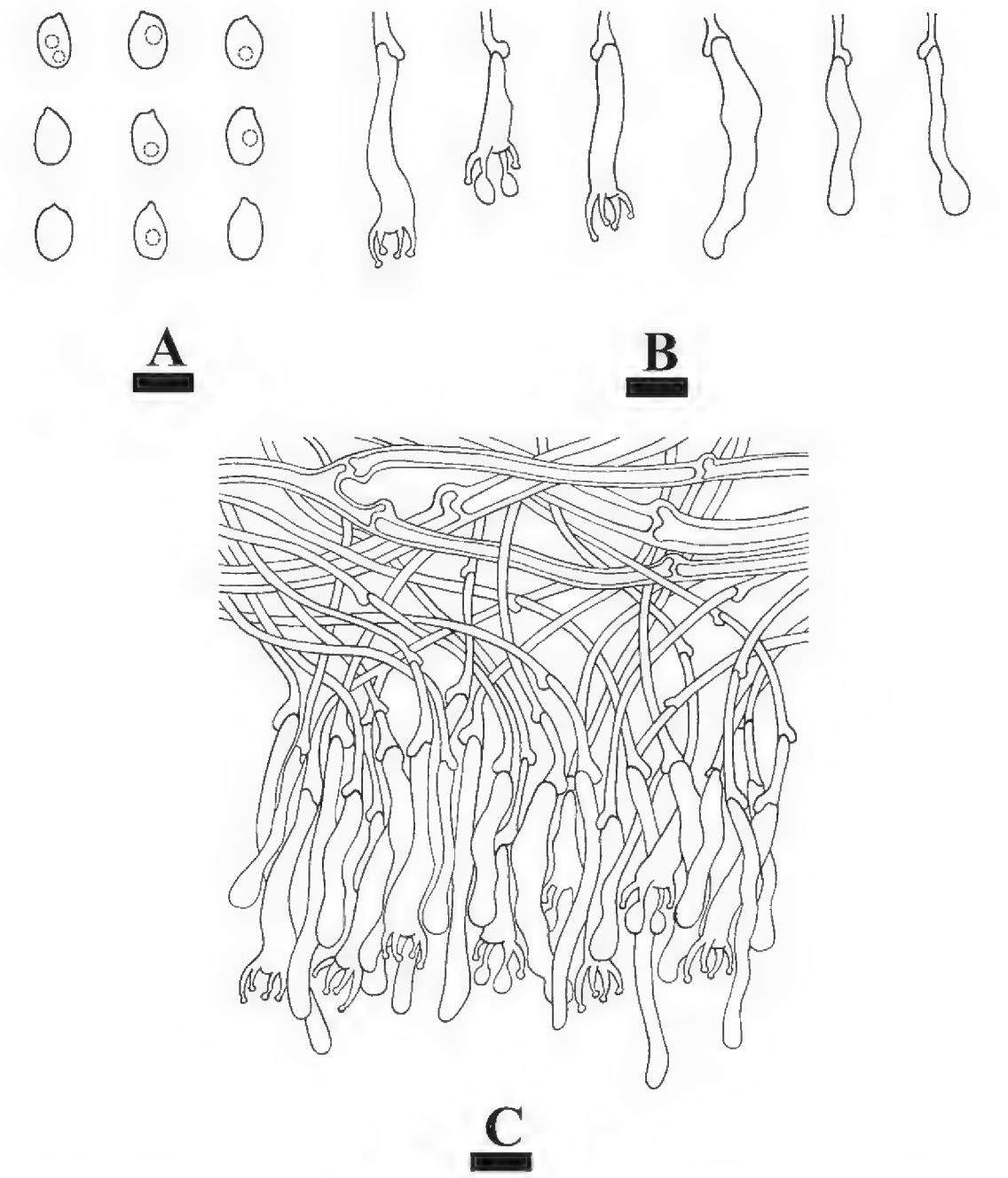

Figure 19. Microscopic structures of *Punctularia nigrodontea* (holotype CLZhao 30592): basidiospores (**A**); basidia and basidioles (**B**); a section of the hymenium (**C**). Scale bars: 10 μm (**A–C**).

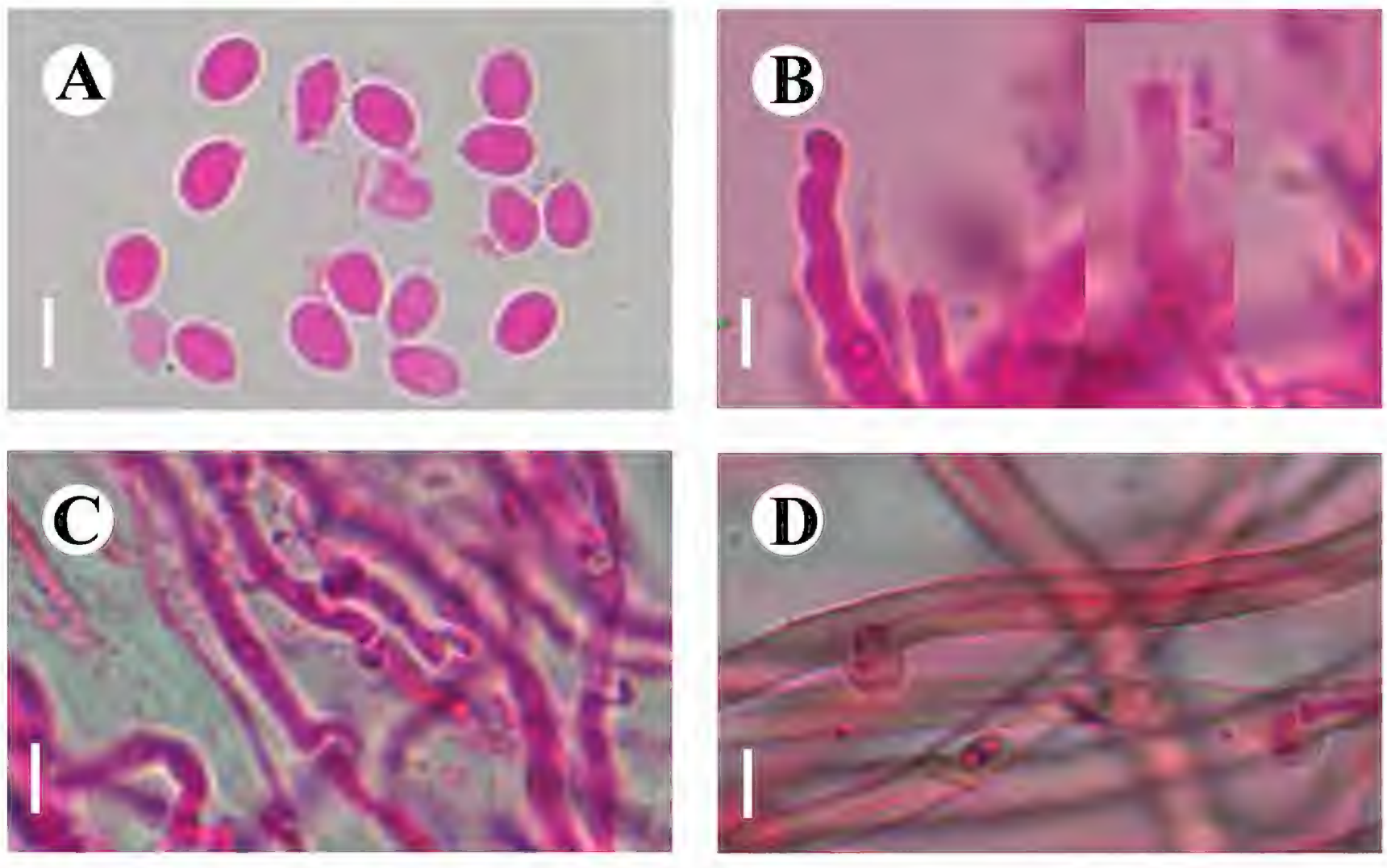

Figure 20. Sections of hymenium of *Punctularia nigrodontea* (holotype CLZhao 30592): basidiospores (**A**); basidia and basidioles (**B**); a section of thin-walled generative hyphae (**C**); a section of thick-walled generative hyphae (**D**). Scale bars: 10 μm (**A–D**); 10 × 100.

Basidiomata. Annual, resupinate to effused-reflexed, adnate but easily separable, gelatinous, without odor or taste when fresh, up to 7 cm long, 3 cm wide, and 600 µm thick. Pileal surface smooth, rigid, fuscous (5/6F5) when fresh, fuscous (5/6F5) to black (51) upon drying; pileal back cushion-shaped grandinioid, rigid, black (51) when fresh, black (51) upon drying. Sterile margin narrow, black (51), up to 1 mm.

Hyphal system. Monomitic; generative hyphae clamp connections, colorless, thin to thick-walled, smooth, rarely branched, interwoven, 3–7 µm in diameter; IKI–, CB–, tissues unchanged in KOH.

Hymenium. Cystidia absent. Basidia clavate, flexuous, with a basal clamp connection and four sterigmata, 16–25 × 3–4.5 µm; basidioles numerous, in shape similar to basidia but smaller.

Spores. Basidiospores ellipsoid, colorless, thin-walled, smooth, IKI–, CB–, 8.5–10(–10.5) × (4.5–)5–6(–6.5) µm, L = 9.24 µm, W = 5.47 µm, Q = 1.69 (n = 30/1).

Discussion

For fungal groups that are difficult to identify based on their morphological features, it is believed (and in most cases also proved) that the application of DNA sequences is able to delimit/recognize species much more easily and unequivocally (Wu et al. 2020; Bhunjun et al. 2024; He et al. 2022, 2024; Hyde et al. 2024a, b; Zhao et al. 2024; Zhou et al. 2024). Over time, understanding different aspects of fungi (i.e., taxonomy, diversity, species number) has improved rapidly by incorporating molecular and bioinformatics tools with traditional approaches (Cui et al. 2019; Wang et al. 2021; Hyde et al. 2023; Zhou et al. 2023; Dong et al. 2024a; Wang et al. 2024a; Wijayawardene et al. 2024).

Phylogenetically, the phylogenetic tree (Figs 1, 2) inferred from ITS+nLSU sequences revealed that the new species *Conferticium albocremeum* was nested into the family Stereaceae within the order Russulales, in which it was retrieved as a sister to *C. heimii*. However, *C. heimii* is distinguished from *C. albocremeum* by having a grayish orange hymenial surface and smaller basidiospores (5.3–6.2 × 3.5–4.2 µm; Wu 1996). Morphologically, *C. fissuratum* and *C. ravum* are similar to *C. albocremeum* by having finely verrucose, ellipsoid, and thin-walled basidiospores (Bernicchia and Gorjón 2010; Shen et al. 2024). However, *C. fissuratum* differs in its tuberculate, rough, white to cream, and cracking hymenial surface and longer subcylindrical cystidia (37–54.5 × 4–8 µm; Shen et al. 2024), and *C. ravum* differs in its smooth, brownish orange to grayish orange hymenial surface and bigger gloeocystidia (30–60 × 6–15 µm; Bernicchia and Gorjón 2010).

Phylogenetically, the multiple genes with ITS+nLSU analysis (Fig. 3) showed that the new species *Dendrocorticiopsis luteoalba* was nested into the family Punctulariaceae within the order Corticiales, and it is closely related with *D. orientalis*. Morphologically, *D. luteoalba* is similar to *D. orientalis* by having clavate apically with resinous cystidia and clavate to subclavate basidia (Wei et al. 2022). However, *D. orientalis* is delimited from *D. luteoalba* by its finely cracked, grayish ivory hymenial surface and smaller, ellipsoid to ovoid basidiospores (5–7 × 3.2–5.2 µm; Wei et al. 2022).

The phylogenetic tree (Figs 4, 5) inferred from ITS+nLSU sequences revealed that *Eichleriella biluoxueshanensis* grouped into the genus *Eichleriella* and clus-

tered into the family Auriculariaceae, in which it was grouped with the clade comprising *E. sinensis*. However, *E. sinensis* is distinguished from *E. biluoxueshanensis* by having narrower basidiospores (10.5–16 × 5.5–7 µm; Li et al. 2023). Morphologically, *E. xinpingensis* C.L. Zhao and *E. yunnanensis* Y.L. Deng & C.L. Zhao are similar to *E. biluoxueshanensis* by all having subcylindrical to allantoid, thin-walled, and smooth basidiospores (Liu et al. 2019; Deng et al. 2024a). However, *E. xinpingensis* differs in its soft, leathery to ceraceous, flesh-pink to clay-pink, and covered by blunt-pointed spines hymenial surface and shorter basidia (15–28 × 5–9 µm; Liu et al. 2019), and *E. yunnanensis* differs in its cream to flesh-pink hymenial surface and smaller basidiospores (7.5–11.5 × 3.5–5 µm; Deng et al. 2024a).

The phylogenetic tree (Fig. 1) inferred from ITS+nLSU sequences revealed that *Gloeohypochnicium yunnanense* grouped into the genus *Gloeohypochnicium* and clustered into the order Russulales, in which it was closely related to *G. analogum*. Morphologically, *G. yunnanense* is similar to *G. analogum* in that it has subglobose, thick-walled, and warted basidiospores (Bernicchia and Gorjón 2010). However, *G. analogum* is delimited from *G. yunnanense* by its coriaceous, cream to ochraceous hymenial surface with a fibrillose margin and smaller gloeocystidia (40–60 × 6–10 µm; Bernicchia and Gorjón 2010).

Based on the ITS+nLSU sequence data (Fig. 3), *Punctularia nigrodontea* was nested into the family Punctulariaceae within the order Corticiales and grouped with the clade comprising *P. atropurpurascens*, *P. bambusicola*, and *P. strigosozonata*. Morphologically, *P. nigrodontea* is similar to *P. atropurpurascens*, *P. bambusicola*, and *P. strigosozonata* by having smooth, thin-walled, and ellipsoid basidiospores (Bernicchia and Gorjón 2010; Guan et al. 2021). However, *P. atropurpurascens* is delimited from *P. nigrodontea* by having the effuse-reflexed and reddish-brown to dark purplish-brown or bluish hymenial surface and larger basidia (40–65 × 5–6 µm; Guan et al. 2021). *Punctularia bambusicola* differs in its resupinate, tuberculate with rose tints, pink to purple hymenial surface, and smaller basidiospores (6.5–8.5 × 3.5–5 µm; Guan et al. 2021). *Punctularia strigosozonata* differs in its resupinate to effuse-reflexed basidiomata with a brown, velutinous margin and longer basidia (40–60 × 4–5 µm; Bernicchia and Gorjón 2010).

Fungi are an ancient, diverse, and heterogeneous group of organisms; they can be found in a wide range of habitats, and play key roles in ecosystems as decomposers, mutualists, and pathogens (Dai et al. 2015, 2021; Cui et al. 2023; Wei 2021; Bhunjun et al. 2022). The Yunnan Province is rich in woody plant species, providing excellent substrates for wood-inhabiting fungi (Dong et al. 2023, 2024a; Wang and Cai 2023; Deng et al. 2024b; Wang et al. 2024b; Zhu et al. 2024). Our study is helpful to further understand the species diversity of wood-inhabiting fungal groups in Yunnan and explore their evolutionary relationships.

Additional information

Conflict of interest

The authors have declared that no competing interests exist.

Ethical statement

No ethical statement was reported.

Funding

The research was supported by the National Natural Science Foundation of China (Project Nos. 32170004) and the High-level Talents Program of Yunnan Province (YNQR-QN-RC-2018-111).

Author contributions

Conceptualization, CZ, AY, and LW; methodology, CZ and LW; software, CZ, YJ, and LW; validation, CZ, SG, and HY; formal analysis, CZ, YJ, and LW; investigation, CZ and LW; resources, CZ; writing – original draft preparation, CZ, AY, LW, and JY; writing – review and editing, CZ and LW; visualization, CZ and LW; supervision, CZ; project administration, CZ; funding acquisition, CZ. All authors have read and agreed to the published version of the manuscript.

Author ORCIDs

Lu Wang https://orcid.org/0009-0004-6274-5953
Changlin Zhao https://orcid.org/0000-0002-8668-1075

Data availability

All of the data that support the findings of this study are available in the main text.

References

Alvarenga RLM, Gibertoni TB (2021) *Crystallodon* Alvarenga gen. nov., a new genus of the Auriculariales from the Neotropics. Cryptogamie. Mycologie 42(2): 17–24. https://doi.org/10.5252/cryptogamie-mycologie2021v42a2

Alvarenga RLM, Spirin V, Malysheva V, Gibertoni TB, Larsson KH (2019) Two new genera and six other novelties in *Heterochaete* sensu lato (Auriculariales, Basidiomycota). Botany 97(8): 439–451. https://doi.org/10.1139/cjb-2019-0046

Bernicchia A, Gorjón SP (2010) Fungi Europaei 12: Corticiaceae s.l.. Edizioni Candusso, Italia.

Bhunjun CS, Niskanen T, Suwannarach N, Wannathes N, Chen YJ, McKenzie EH, Maharachchikumbura SS, Buyck B, Zhao CL, Fan YG, Zhang JY, Dissanayake AJ, Marasinghe DS, Jayawardena RS, Kumla J, Padamsee M, Chen Y-Y, Liimatainen K, Ammirati JF, Phukhamsakda C, Liu J-K, Phonrob W, Randrianjohany É, Hongsanan S, Cheewangkoon R, Bundhun D, Khuna S, Yu W-J, Deng L-S, Lu Y-Z, Hyde KD, Lumyong S (2022) The numbers of fungi: Are the most speciose genera truly diverse? Fungal Diversity 114(1): 387–462. https://doi.org/10.1007/s13225-022-00501-4

Bhunjun CS, Chen YJ, Phukhamsakda C, Boekhout T, Groenewald JZ, McKenzie EHC, Francisco EC, Frisvad JC, Groenewald M, Hurdeal VG, Luangsa-ard J, Perrone G, Visagie CM, Bai FY, Błaszkowski J, Braun U, de Souza FA, de Queiroz MB, Dutta AK, Gonkhom D, Goto BT, Guarnaccia V, Hagen F, Houbraken J, Lachance MA, Li JJ, Luo KY, Magurno F, Mongkolsamrit S, Robert V, Roy N, Tibpromma S, Wanasinghe DN, Wang DQ, Wei DP, Zhao CL, Aiphuk W, Ajayi-Oyetunde O, Arantes TD, Araujo JC, Begerow D, Bakhshi M, Barbosa RN, Behrens FH, Bensch K, Bezerra JDP, Bilański P, Bradley CA, Bubner B, Burgess TI, Buyck B, Čadež N, Cai L, Calaça FJS, Campbell LJ, Chaverri P, Chen YY, Chethana KWT, Coetzee B, Costa MM, Chen Q, Custódio FA, Dai YC, Damm U, de Azevedo SALCM, De Miccolis Angelini RM, Dijksterhuis J, Dissanayake AJ, Doilom

M, Dong W, Alvarez-Duarte E, Fischer M, Gajanayake AJ, Gené J, Gomdola D, Gomes AAM, Hausner G, He MQ, Hou L (2024) What are the 100 most cited fungal genera? Studies in Mycology 108: 1–411. https://doi.org/10.3114/sim.2024.108.01

Cui BK, Li HJ, Ji X, Zhou JL, Song J, Si J, Yang ZL, Dai YC (2019) Species diversity, taxonomy and phylogeny of Polyporaceae (Basidiomycota) in China. Fungal Diversity 97(1): 137–392. https://doi.org/10.1007/s13225-019-00427-4

Cui BK, Pan XH, Pan F, Sun YF, Xing JH, Dai YC (2023) Species diversity and resources of *Ganoderma* in China. Junwu Xuebao 42(1): 170–178.

Dai YC, Cui BK, Si J, He SH, Hyde KD, Yuan HS, Liu XY, Zhou LW (2015) Dynamics of the worldwide number of fungi with emphasis on fungal diversity in China. Mycological Progress 14(8): 62. https://doi.org/10.1007/s11557-015-1084-5

Dai LD, Wu SH, Nakasone KK, Burdsall Jr HH, He SH (2017) Two new species of *Aleurodiscus* s.l. (Russulales, Basidiomycota) on bamboo from tropics. Mycoscience 58(3): 213–220. https://doi.org/10.1016/j.myc.2017.02.001

Dai YC, Yang ZL, Cui BK, Wu G, Yuan HS, Zhou LW, He SH, Ge ZW, Wu F, Wei YL, Yuan Y, Si J (2021) Diversity and systematics of the important macrofungi in Chinese forests. Junwu Xuebao 40(4): 770–805. https://doi.org/10.13346/j.mycosystema.210036

Deng YL, Chen M, Liu LF, Zhao R, Li Q, Miao JY, Zhao CL, Zhou HM (2024a) Molecular phylogeny and morphology reveal a new *Eichleriella* species (Auriculariales, Basidiomycota) from China. Phytotaxa 675(3): 247–260. https://doi.org/10.11646/phytotaxa.675.3.4

Deng YL, Jabeen S, Zhao CL (2024b) Species diversity and taxonomy of *Vararia* (Russulales, Basidiomycota) with descriptions of six species from southwestern China. MycoKeys 103: 97–128. https://doi.org/10.3897/mycokeys.103.118980

DePriest PT, Sikaroodi M, Lawrey JD, Diederich P (2005) *Marchandiomyces lignicola* sp. nov. shows recent and repeated transition between a lignicolous and a lichenicolous habit. Mycological Research 109(1): 57–70. https://doi.org/10.1017/S0953756204001601

Dong JH, Gu JY, Zhao CL (2023) Diversity of wood-decaying fungi in Wenshan Area, Yunnan Province, China. Junwu Xuebao 42(3): 638–662. https://doi.org/10.13346/j.mycosystema.220205

Dong JH, Li Q, Yuan Q, Luo YX, Zhang XC, Dai YF, Zhou Q, Liu XF, Deng YL, Zhou HM, Zhao CL, Akmal M (2024a) Species diversity, taxonomy, molecular systematics and divergence time of wood-inhabiting fungi in Yunnan-Guizhou Plateau, Asia. Mycosphere : Journal of Fungal Biology 15(1): 1110–1293. https://doi.org/10.5943/mycosphere/15/1/10

Dong JH, Zhu YG, Qian CB, Zhao CL (2024b) Taxonomy and phylogeny of Auriculariales (Agaricomycetes, Basidiomycota) with descriptions of four new species from southwestern China. MycoKeys 108: 115–146. https://doi.org/10.3897/mycokeys.108.128659

Felsenstein J (1985) Confidence intervals on phylogenetics: An approach using bootstrap. Evolution; International Journal of Organic Evolution 39(4): 783–791. https://doi.org/10.2307/2408678

Fukami T, Dickie IA, Wilkie JP, Paulus BC, Park D, Roberts A, Buchanan PK, Allen RB (2010) Assembly history dictates ecosystem functioning: Evidence from wood decomposer communities. Ecology Letters 13(6): 675–684. https://doi.org/10.1111/j.1461-0248.2010.01465.x

Ghobad-Nejhad M, Duhem B (2014) Novelties in the Corticiales: *Vuilleminia nilsii* sp. nov. and *Dendrominia* gen. nov. (Basidiomycota). Mycological Progress 13(1): 1–11. https://doi.org/10.1007/s11557-012-0881-3

Ghobad-Nejhad M, Ginns J (2012) *Vuilleminia erastii* sp. nov. (Corticiales), an amphi-Beringian species and revision of the occurrence of *Vuilleminia comedens* in North America. Mycoscience 53(4): 290–299. https://doi.org/10.1007/S10267-011-0168-6

Ghobad-Nejhad M, Nilsson RH, Hallenberg N (2010) Phylogeny and taxonomy of the genus *Vuilleminia* (Basidiomycota) based on molecular and morphological evidence, with new insights into Corticiales. Taxon 59(5): 1519–1534. https://doi.org/10.1002/tax.595016

Ghobad-Nejhad M, Langer E, Nakasone K, Diederich P, Nilsson RH, Rajchenberg M, Ginns J (2021) Digging up the roots: Taxonomic and phylogenetic disentanglements in Corticiaceae s.s. (Corticiales, Basidiomycota) and Evolution of Nutritional Modes. Frontiers in Microbiology 2320: e704802. https://doi.org/10.3389/fmicb.2021.704802

Gorjón SP, Bernicchia A (2017) *Dendrocorticium pinsapineum* (Corticiales, Basidiomycota), second world distributional area in Italy. Nova Hedwigia 105(3–4): 341–346. https://doi.org/10.1127/nova_hedwigia/2017/0415

Gorjón S, Greslebin A (2024) *Stereodiscus pseudotrivialis* (Russulales, Basidiomycota), a new species from the Patagonian Andes of Argentina. Phytotaxa 636(2): 152–162. https://doi.org/10.11646/phytotaxa.636.2.4

Guan QX, Liu CM, Zhao TJ, Zhao CL (2020) *Heteroradulum yunnanensis* sp. nov. (Auriculariales, Basidiomycota) evidenced by morphological characters and phylogenetic analyses in China. Phytotaxa 437(2): 51–59. https://doi.org/10.11646/phytotaxa.437.2.1

Guan QX, Zhao W, Zhao CL (2021) A new species of *Punctularia* (Punctulariaceae, Basidiomycota) from southwest China. Phytotaxa 489(3): 285–292. https://doi.org/10.11646/phytotaxa.489.3.5

He SH, Vlasak J, Dai YC (2014) *Hispidaedalea* gen. nov and *Griseoporia taiwanense* sp. nov (Gloeophyllales, Basidiomycota) based on morphological and molecular characters. Mycological Progress 13(3): 833–839. https://doi.org/10.1007/s11557-014-0966-2

He MQ, Zhao RL, Liu MD, Denchev TT, Begerow D, Yurkov A, Kemler M, Millanes AM, Wedin M, McTaggart AR, Shivas RG, Buyck B, Chen J, Vizzini A, Papp V, Zmitrovich IV, Davoodian N, Hyde KD (2022) Species diversity of Basidiomycota. Fungal Diversity 114(1): 1–45. https://doi.org/10.1007/s13225-021-00497-3

He MQ, Cao B, Liu F, Boekhout T, Denchev TT, Power N, Denchev CM, Kemler M, Gorjón SP, Begerow D, Valenzuela R, Davoodian N, Niskanen T, Vizzini A, Redhead SA (2024) Phylogenomics, divergence times and notes of orders in Basidiomycota. Fungal Diversity 126(3): 1–280. https://doi.org/10.1007/s13225-024-00535-w

Hood IA, McDougal RL, Somchit C, Kimberley MO, Lewis AS, Hood JO (2018) Fungi decaying the wood of fallen beech (Nothofagus) trees in the South Island of New Zealand. Canadian Journal of Forest Research 49(1): 1–17. https://doi.org/10.1139/cjfr-2018-0179

Hu Y, Karunarathna SC, Li H, Galappaththi MC, Zhao CL, Kakumyan P, Mortimer PE (2022) The impact of drying temperature on basidiospore size. Diversity 14(4): 239. https://doi.org/10.3390/d14040239

Hyde KD, Amuhenage TB, Apurillo CCS, Asghari R, Aumentado HD, Bahkali AH, Bera I, Bhunjun CS, Calabon MS, Chandrasiri S, Chethana KWT, Doilom M, Dong W, Fallahi M, Gajanayake AJ, Gomdola D, Gunarathne A, Hongsanan S, Huanraluek N, Jayawardena

RS, Kapov SA, Khyaju S, Le L, Li CJY, Li QR, Li YX, Lin CG, Linn MM, Liu JK, Liu NG, Luangharn T, Madagammana AD, Manawasinghe IS, Marasinghe DS, McKenzie EHC, Meakala N, Meng QF, Mukhopadhyay S, Norphanphoun C, Pem D, Phukhamsakda C, Sarma VV, Selcuk F, Senanayake IC, Shah S, Shu YX, Silva HVS, Su HL, Tavakol M, Thakshila SAD, Thiyagaraja V, Thongklang N, Tian Q, Tibpromma S, Tun ZL, Ulukapi M, Wang Y, Wannasawang N, Wijayawardene NN, Wimalasena SDMK, Xiao Y, Xiong YR, Yasanthika WAE, Li Q, Dai DQ (2023) Fungalpedia, an illustrated compendium for the fungi and fungus-like taxa. Mycosphere: Journal of Fungal Biology 14(1): 1835–1959. https://doi.org/10.5943/mycosphere/14/1/22

Hyde KD, Baldrian P, Chen Y, Chethana KWT, De Hoog S, Doilom M, Gomes de Farias AR, Gonçalves MFM, Gonkhom D, Gui H, Hilário S, Hu Y, Jayawardena RS, Khyaju S, Kirk PM, Kohout P, Luangharn T, Maharachchikumbura SSN, Manawasinghe IS, Mortimer PE, Niego AGT, Phonemany M, Sandargo B, Senanayake IC, Stadler M, Surup F, Thongklang N, Wanasinghe DN, Bahkali AH, Walker A (2024a) Current trends, limitations and future research in the fungi? Fungal Diversity 125(1): 1–71. https://doi.org/10.1007/s13225-023-00532-5

Hyde KD, Saleh A, Aumentado HDR, Boekhout T, Bera I, Khyaju S, Bhunjun CS, Chethana KWT, Phukhamsakda C, Doilom M, Thiyagaraja V, Mortimer PE, Maharachchikumbura SSN, Hongsanan S, Jayawardena RS, Dong W, Jeewon R, Al-Otibi F, Wijesinghe SN, Wanasinghe DN (2024b) Fungal numbers: Global needs for a realistic assessment. Fungal Diversity 128(1): 1–36. https://doi.org/10.1007/s13225-023-00532-5

Ji XH, Sun B, He G, Sun QB (2024) *Scytinostroma bambusinum* sp. nov. (Russulales, Basidiomycota) in China evidenced by morphological characteristics and phylogenetic analyses. Biodiversity Data Journal 12: e115975. https://doi.org/10.3897/BDJ.12.e115975

Katoh K, Rozewicki J, Yamada KD (2019) MAFFT online service: Multiple sequence alignment, interactive sequence choice and visualization. Briefings in Bioinformatics 20(4): 1160–1166. https://doi.org/10.1093/bib/bbx108

Knijn A, Ferretti A (2018) *Punctularia atropurpurascens* in the Villa Ada urban Park in Rome, Italy. Mycology 47: 29–39. https://doi.org/10.6092/issn.2531-7342/8349

Kneal RJ, Smith ME (2015) *Artomyces nothofagi* sp. nov., a clavarioid fungus from a Chilean Nothofagus forest. Mycotaxon 130(3): 653–660. https://doi.org/10.5248/130.653

Larsson A (2014) AliView: A fast and lightweight alignment viewer and editor for large data sets. Bioinformatics (Oxford, England) 30(22): 3276–3278. https://doi.org/10.1093/bioinformatics/btu531

Larsson E, Larsson KH (2003) Phylogenetic relationships of russuloid basidiomycetes with emphasis on aphyllophoralean taxa. Mycologia 95(6): 1037–1065. https://doi.org/10.1080/15572536.2004.11833020

Li QZ, Liu SL, Wang XW, May TW, Zhou LW (2022) Redelimitation of *Heteroradulum* (Auriculariales, Basidiomycota) with *H. australiense* sp. nov. MycoKeys 86: 87–101. https://doi.org/10.3897/mycokeys.86.76425

Li Y, Nie T, Nakasone KK, Li HJ, He SH (2023) Taxonomy and phylogeny of corticioid fungi in Auriculariaceae (Auriculariales, Basidiomycota): A new genus, five new species and four new combinations. Journal of Fungi (Basel, Switzerland) 9(3): 318. https://doi.org/10.3390/jof9030318

Liu XF, Shen S, Zhao CL (2019) Morphological and molecular identification of a new species of *Eichleriella* (Auriculariales, Basidiomycota) in China. Phytotaxa 404(6): 245–254. https://doi.org/10.11646/phytotaxa.404.6.3

Liu SL, Shen ZQ, Li QZ, Liu XY, Zhou LW (2022) *Alloexidiopsis* gen. nov., a revision of generic delimitation in Auriculariales (Basidiomycota). Frontiers in Microbiology 13: 894641. https://doi.org/10.3389/fmicb.2022.894641

Lücking R, Moncada B (2017) Dismantling *Marchandiomphalina* into *Agonimia* (Verrucariaceae) and *Lawreymyces* gen. nov. (Corticiaceae): Setting a precedent to the formal recognition of thousands of voucherless fungi based on type sequences. Fungal Diversity 84(1): 119–138. https://doi.org/10.1007/s13225-017-0382-4

Lücking R, Aime MC, Robbertse B, Miller AN, Aoki T, Ariyawansa HA, Cardinali G, Crous PW, Druzhinina IS, Geiser DM, Hawksworth DL, Hyde KD, Irinyi L, Jeewon R, Johnston PR, Kirk PM, Malosso E, May TW, Meyer W, Nilsson HR, Öpik M, Robert V, Stadler M, Thines M, Vu D, Yurkov AM, Zhang N, Schoch CL (2021) Fungal taxonomy and sequence-based nomenclature. Nature Microbiology 6(5): 1–9. https://doi.org/10.1038/s41564-021-00888-x

Maekawa N, Sugawara R, Kogi H, Norikura S, Sotomea K, Endoa N, Nakagiria A, Ushijima S (2023) *Hypochnicium* sensu lato (Polyporales, Basidiomycota) from Japan, with descriptions of a new genus and three new species. Mycoscience 64(1): 19–34. https://doi.org/10.47371/mycosci.2022.10.001

Malysheva V, Spirin V (2017) Taxonomy and phylogeny of the Auriculariales (Agaricomycetes, Basidiomycota) with stereoid basidiocarps. Fungal Biology 121(8): 689–715. https://doi.org/10.1016/j.funbio.2017.05.001

Malysheva V, Spirin V, Miettinen O, Motato-Vásquez V, Hernawati JSSS, Larsson KH (2018) Revision of *Protohydnum* (Auriculariales, Basidiomycota). Mycological Progress 17(7): 805–814. https://doi.org/10.1007/s11557-018-1393-6

Miettinen O, Spirin V, Niemelä T (2012) Notes on the genus *Aporpium* (Auriculariales, Basidiomycota), with a new species from temperate Europe. Annales Botanici Fennici 49(5–6): 359–368. https://doi.org/10.5735/085.049.0607

Miller MA, Pfeiffer W, Schwartz T (2012) The CIPRES science gateway. Proceedings of the 1st Conference of the Extreme Science and Engineering Discovery Environment: Bridging from the Extreme to the Campus and Beyond. Chicago, IL, 39 pp. https://doi.org/10.1145/2335755.2335836

Nylander JAA (2004) *MrModeltest v2.* Program distributed by the author. Evolutionary Biology Centre, Uppsala University.ampignons de l'Équateur (Pugillus IV). Bulletin de l'Herbier Boissier 3: 53–74.

Petersen JH (1996) Farvekort. The Danish Mycological Society's Colour-Chart. Foreningen til Svampekundskabens Fremme, Greve, Germany, 6 pp.

Qin GF, Qin WM, Wang HC, Zhao J, Korhonen K, Chen J, Dai YC, Yuan Y (2024) Phylogeny and species diversity of *Armillaria* in China based on morphological, mating test, and GCPSR criteria. Mycology 1–35. https://doi.org/10.1080/21501203.2024.2404121

Ronquist F, Teslenko M, van der Mark P, Ayres DL, Darling A, Höhna S, Larget B, Liu L, Suchard MA, Huelsenbeck JP (2012) Mrbayes 3.2: Efficient Bayesian phylogenetic inference and model choice across a large model space. Systematic Biology 61(3): 539–542. https://doi.org/10.1093/sysbio/sys029

Shen LL, Wang KY, Xia H, Lang SL, Yao L, Yang X (2024) Molecular phylogeny and morphology reveal a new wood-inhabiting fungal species of *Conferticium* (Stereaceae, Basidiomycota) from southwest China. Phytotaxa 677(1): 77–86. https://doi.org/10.11646/phytotaxa.677.1.4

Sotome K, Maekawa N, Nakagiri A, Lee SS, Hattori T (2014) Taxonomic study of Asian species of poroid Auriculariales. Mycological Progress 13(4): 987–997. https://doi.org/10.1007/s11557-014-0984-0

Spirin V, Malysheva V, Larsson KH (2018) On some forgotten of *Exidia* and *Myxarium* (Auriculariales, Basidiomycota). Nordic Journal of Botany 36(3): e01601. https://doi.org/10.1111/njb.01601

Spirin V, Volobuev S, Malysheva V, Miettinen O, Kotiranta H, Larsson KH (2021) Identity of the subalpine–subarctic corticioid fungus *Megalocystidium leucoxanthum* (Russulales, Basidiomycota) and six related species. Plant Ecology and Evolution 154(2): 231–244. https://doi.org/10.5091/plecevo.2021.1857

Stroheker S, Weiss M, Sieber TN, Bugmann H (2018) Ecological factors influencing Norway *Spruce* regeneration on nurse logs in a subalpine virgin forest. Forests 9(3): 120. https://doi.org/10.3390/f9030120

Swofford DL (2002) PAUP*: Phylogenetic analysis using parsimony (*and Other Methods), Version 4.0b10. Sinauer Associates: Sunderland, MA, USA.

Tian Y, Ghobad-Nejhad M, He SH, Dai YC (2018) Three new species of *Aleurodiscus* s.l. (Russulales, Basidiomycota) from southern China. MycoKeys 37: 93–107. https://doi.org/10.3897/mycokeys.37.25901

Tohtirjap A, Hou SX, Rivoire B, Gates G, Wu F, Dai YC (2023) Two new species of *Exidia* sensu lato (Auriculariales, Basidiomycota) based on morphology and DNA sequences. Frontiers in Microbiology 13: 1080290. https://doi.org/10.3389/fmicb.2022.1080290

Vilgalys R, Hester M (1990) Rapid genetic identification and mapping of enzymatically amplified ribosomal DNA from several *Cryptococcus* species. Journal of Bacteriology 172(8): 4238–4246. https://doi.org/10.1128/jb.172.8.4238-4246.1990

Vu D, Groenewald M, de Vries M, Gehrmann T, Stielow B, Eberhardt U, Al-Hatmi A, Groenewald JZ, Cardinali G, Houbraken J, Boekhout T, Crous PW, Robert V, Verkley GJM (2019) Large-scale generation and analysis of filamentous fungal DNA barcodes boosts coverage for kingdom fungi and reveals thresholds for fungal species and higher taxon delimitation. Studies in Mycology 92(1): 135–154. https://doi.org/10.1016/j.simyco.2018.05.001

Wang K, Cai L (2023) Overview of the historical and current status of fungal taxonomy and diversity in China. Junwu Xuebao 42(1): 50–62. https://doi.org/10.13346/j.mycosystema.220497

Wang YR, Wu YD, Vlasák J, Yuan Y, Dai YC (2021) Phylogenetic analysis demonstrating four new species in *Megasporoporia* sensu lato (Polyporales, Basidiomycota). Mycosphere: Journal of Fungal Biology 12(1): 1012–1037. https://doi.org/10.5943/mycosphere/12/1/11

Wang CG, Zhao H, Liu HG, Zeng GY, Yuan Y, Dai YC (2023) A multi-gene phylogeny clarifies species diversity, taxonomy, and divergence times of *Ceriporia* and other related genera in Irpicaceae (Polyporales, Basidiomycota). Mycosphere: Journal of Fungal Biology 14(1): 1665–1729. https://doi.org/10.5943/mycosphere/14/1/19

Wang CG, Dai YC, Kout J, Gates GM, Liu HG, Yuan Y, Vlasák J (2024a) Multi-gene phylogeny and taxonomy of *Physisporinus* (Polyporales, Basidiomycota). Mycosphere: Journal of Fungal Biology 15(1): 1455–1521. https://doi.org/10.5943/mycosphere/15/1/12

Wang L, Yang X, Zhao CL (2024b) The wood-decaying fungal diversity unveiled by morphology and phylogeny in Ailaoshan Mountain, Yunnan, China. Phytotaxa 661(1): 001–030. https://doi.org/10.11646/phytotaxa.661.1.1

Wei YL (2021) Forming mechanisms and ecological function of wood-decaying fungal community in forest ecosystem. Shengtaixue Zazhi 40(2): 534–543. https://doi.org/10.13292/j.1000-4890.202102.001

Wei CL, Chen CC, He SH, Wu SH (2022) *Dendrocorticiopsis orientalis* gen. et sp. nov. of the Punctulariaceae (Corticiales, Basidiomycota) revealed by molecular data. MycoKeys 90: 19–30. https://doi.org/10.3897/mycokeys.90.84562

Weiß M, Oberwinkler F (2001) Phylogenetic relationships in Auriculariales and related groups – Hypotheses derived from nuclear ribosomal DNA sequences. Mycological Research 105(4): 403–415. https://doi.org/10.1017/S095375620100363X

White TJ, Bruns T, Lee S, Taylor J (1990) Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In: Innis MA, Gelfand DH, Sninsky JJ, White TJ (Eds) PCR protocols: A guide to methods and applications. Academic Press, San Diego, 315–322. https://doi.org/10.1016/B978-0-12-372180-8.50042-1

Wijayawardene NN, Hyde KD, Dai DQ, Sánchez-García M, Goto BT, Saxena RK, Erdoğdu M, Selçuk F, Rajeshkumar KC, Aptroot A, Błaszkowski J, Boonyuen N, da Silva GA, de Souza FA, Dong W, Ertz D, Haelewaters D, Jones EBG, Karunarathna SC, Kirk PM, Kukwa M, Kumla J, Leontyev DV, Lumbsch HT, Maharachchikumbura SSN, Marguno F, Martínez-Rodríguez P, Mešić A, Monteiro JS, Oehl F, Pawłowska J, Pem D, Pfiegler WP, Phillips AJL, Pošta A, He MQ, Li JX, Raza M, Sruthi OP, Suetrong S, Suwannarach N, Tedersoo L, Thiyagaraja V, Tibpromma S, Tkalčec Z, Tokarev YS, Wanasinghe DN, Wijesundara DSA, Wimalaseana SDMK, Madrid H, Zhang GQ, Gao Y (2022) Outline of Fungi and fungus-like taxa – 2021. Mycosphere: Journal of Fungal Biology 13(1): 53–453. https://doi.org/10.5943/mycosphere/13/1/2

Wijayawardene NN, Hyde KD, Mikhailov KV, Péter G, Aptroot A, Pires-Zottarelli CLA, Goto BT, Tokarev YS, Haelewaters D, Karunarathna SC, Kirk PM, Santiago ALCMA, Saxena RK, Schoutteten N, Wimalasena MK, Aleoshin VV, Al-Hatmi AMS, Ariyawansa KGSU, Assunção AR, Bamunuarachchige TC, Baral HO, Bhat DJ, Blaszkowski J, Boekhout T, Boonyuen N, Brysch-Herzberg M, Cao B, Cazabonne J, Chen XM, Coleine C, Dai DQ, Daniel HM, Silva SBG, Souza FA, Dolatabadi S, Dubey MK, Dutta AK, Ediriweera A, Egidi E, Elshahed MS, Fan XL, Felix JRB, Galappaththi MCA, Groenewald M, Han L-S, Huang B, Hurdeal VG, Ignatieva AN, Jerônimo GH, Jesus AL, Kondratyuk S, Kumla J, Kukwa M, Li QR, Lima JLR, Liu XY, Lu WH, Lumbsch HT, Madrid H, Magurno F, Marson G, McKenzie EHC, Menkis A, Mešić A, Nascimento ECR, Nassonova ES, Nie Y, Oliveira NVL, Ossowska EA, Pawtowska J, Peintner U, Pozdnyakov LR, Premarathne BM, Priyashantha AKH, Quandt CA, Queiroz MB, Rajeshkuma KC, Raza M, Roy N, Samarakoon MC, Santos AA, Santos LA, Schumm F, Selbmann L, Selçuk F, Simmons DR, Simakova AV, Smith MT, Sruthi OP, Suwannarach N, Tanaka K, Tibpromma S, Tomás EO, Ulukapı M, Vooren NV, Wanasinghe DN, Weber E, Wu QZ, Yang EF, Yoshioka R, Youssef NH, Zandijk A, Zhang GQ, Zhang JY, Zhao H, Zhao RL, Zverkov OA, Thines M, Karpov SA (2024) Classes and phyla of the kingdom Fungi. Fungal Diversity 127(1): 1–165. https://doi.org/10.1007/s13225-024-00540-z

Wu SH (1996) Studies on *Gloeocystidiellum* sensu lato (Basidiomycotina) in Taiwan. Mycotaxon 58: 1–68.

Wu SH, Hibbett DS, Binder M (2001) Phylogenetic analyses of *Aleurodiscus* s.l. and allied genera. Mycologia 93(4): 720–731. https://doi.org/10.1080/00275514.2001.12063203

Wu F, Yuan Y, Chen JJ, Cui BK, Zhou M, Dai YC (2020) Terrestriporiaceae fam. nov., a new family of Russulales (Basidiomycota). Mycosphere: Journal of Fungal Biology 11(1): 2755–2766. https://doi.org/10.5943/mycosphere/11/1/21

Wu F, Zhou LW, Vlasák J, Dai YC (2022) Global diversity and systematics of Hymenochaetaceae with poroid hymenophore. Fungal Diversity 113(1): 1–192. https://doi.org/10.1007/s13225-021-00496-4

Ye SY, Zhang YB, Wu F, Liu HX (2020) Multi-locus phylogeny reveals two new species of *Exidia* (Auriculariales, Basidiomycota) from China. Mycological Progress 19(9): 859–868. https://doi.org/10.1007/s11557-020-01601-8

Yuan HS, Lu X, Decock C (2018) Molecular and morphological evidence reveal a new genus and species in Auriculariales from tropical China. MycoKeys 35: 27–39. https://doi.org/10.3897/mycokeys.35.25271

Yuan Y, Chen JJ, Korhonen K, Martin F, Dai YC (2021) An updated global species diversity and phylogeny in the forest pathogenic genus Heterobasidion (Basidiomycota, Russulales). Frontiers in Microbiology 11: 596393. https://doi.org/10.3389/fmicb.2020.596393

Yuan Y, Bian LS, Wu YD, Chen JJ, Wu F, Liu HG, Zeng GY, Dai YC (2023) Species diversity of pathogenic wood-rotting fungi (Agaricomycetes, Basidiomycota) in China. Mycology 14(1): 204–226. https://doi.org/10.1080/21501203.2023.2238779

Zhang QY, Liu HG, Bian LS, Chen Q (2023) Two new species of *Scytinostroma* (Russulales, Basidiomycota) in Southwest China. Frontiers in Cellular and Infection Microbiology 13: 1189600. https://doi.org/10.3389/fcimb.2023.1189600

Zhao CL, Wu ZQ (2017) *Ceriporiopsis kunmingensis* sp. nov. (Polyporales, Basidiomycota) evidenced by morphological characters and phylogenetic analysis. Mycological Progress 16(1): 93–100. https://doi.org/10.1007/s11557-016-1259-8

Zhao CL, Qu MH, Huang RX, Karunarathna SC (2023) Multi-gene phylogeny and taxonomy of the wood-rotting fungal genus *Phlebia* sensu lato (Polyporales, Basidiomycota). Journal of Fungi (Basel, Switzerland) 9(3): 320. https://doi.org/10.3390/jof9030320

Zhao H, Wu YD, Yang ZR, Liu HG, Wu F, Dai YC, Yuan Y (2024) Polypore funga and species diversity in tropical forest ecosystems of Africa, America and Asia, and a comparison with temperate and boreal regions of the Northern Hemisphere. Forest Ecosystems 11: 100200. https://doi.org/10.1016/j.fecs.2024.100200

Zhou LW, Dai YC (2013) Taxonomy and phylogeny of wood-inhabiting hydnoid species in Russulales two new genera, three new species and two new combinations. Mycologia 105(3): 636–649. https://doi.org/10.3852/12-011

Zhou M, Chen JJ, Vlasák J, Yuan Y (2021) *Dentipellicula guyanensis* sp. nov. (Hericiaceae, Basidiomycota) from French Guiana. Phytotaxa 478(2): 261–267. https://doi.org/10.11646/phytotaxa.478.2.7

Zhou M, Dai YC, Vlasák J, Liu HG, Yuan Y (2023) Updated systematics of Trichaptum s.l. (Hymenochaetales, Basidiomycota). Mycosphere: Journal of Fungal Biology 14(1): 815–917. https://doi.org/10.5943/mycosphere/14/1/11

Zhou HM, Dai YC, Bian LS, Liu HG, Vlasák J, Yuan Y (2024) Diversity, divergence time, and biogeography of the genus *Albatrellus* (Agaricomycetes, Russulales). Mycology 1–39. https://doi.org/10.1080/21501203.2024.2386021

Zhu AH, Zhang QY, Luo KY, He SH, Ma HX (2024) Diversity of wood-inhabiting macrofungi in tropical areas of Yunnan Province, China. Junwu Xuebao 43(3): 230265. https://doi.org/10.13346/j.mycosystema.230265